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OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 05:22:44 ; Search time 10357.4 Seconds
(without alignments)
7013.028 Million cell updates/sec

Title: US-09-937-636-1

Perfect score: 1536

Sequence: 1 atgctactgccaactgctgct.....atgcagaagtcgaagtccaa 1536

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_cm:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

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9: gb_pr:*

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11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1244.8	81.0	3124	9 AF311905	Homo sapi
2	1100.4	71.6	2374	6 CO842614	Sequence
3	1100.4	71.6	2374	9 AK122619	Homo sapi
4	1082	70.4	2565	6 AX355516	Sequence
5	1078.8	70.2	2764	6 CQ757791	Sequence
6	1078.8	70.2	2764	6 AX376050	Sequence
7	1078.8	70.2	2764	6 AY358337	Homo sapi
8	956.2	62.3	2208	6 AX365530	Sequence
9	956.2	62.3	3012	9 AF301007	Homo sapi
10	956.2	62.3	3024	6 AX355542	Sequence
11	954.6	62.1	2176	9 AF310233	Homo sapi
12	869.2	56.6	2321	6 AX497858	Sequence
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17	777.4	50.6	2295	6 BD251703	Sequence
18	740.8	48.2	2076	6 CQ734422	Sequence
19	738	48.0	2954	6 AX365517	Sequence

20 733.6 47.8 1665 6 AX365519 Sequence
21 686.8 44.7 2154 5 AX430336 Sequence
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23 620.6 40.4 2448 9 AX358135 Homo sapi
24 619 40.3 2273 9 AB072038 Homo sapi
25 610.6 39.8 2052 6 AX365546 Sequence
26 593 38.4 2605 9 BC039008 Homo sapi
27 590.2 38.4 2823 6 AX365518 Sequence
28 562 36.6 1344 6 BD261712 12 human
29 529 34.4 8400 9 AY029277 Homo sapi
30 529 34.4 143045 9 AC008750 Homo sapi
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33 482.8 31.4 3994 9 AL162428 Human DNA
34 482.8 31.4 141663 2 AL356633 Homo sapi
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39 402.8 26.2 469 6 BD261739 12 human
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ALIGNMENTS

RESULT 1
AF311905
LOCUS AF311905 3124 bp mRNA linear PRI 21-AUG-2001
DEFINITION Homo sapiens sialic acid-binding Ig-like lectin 10 (SIGLEC10) mRNA, complete cds.
ACCESSION AF311905
VERSION AF311905.1 GI:15217165
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3124)
AUTHORS Li,N., Zhang,W., Wan,T., Zhang,J., Chen,T., Yu,Y., Wang,J. and Cao,X.
TITLE Cloning and characterization of Siglec-10, a novel sialic acid binding member of the Ig superfamily, from human dendritic cells
J. Biol. Chem. 276 (30), 28106-28112 (2001)
MEDLINE 21359381
PubMed 11358961
REFERENCE 2 (bases 1 to 3124)
AUTHORS Li,N., Zhang,W., Wan,T. and Cao,X.
TITLE Direct Submission
Submitted (15-AUG-2001) Department of Immunology, Second Military Medical University, 800 Xiangyin Rd., Shanghai 200433, P.R.China
JOURNAL
FEATURES
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S.,
Yamamoto, J., Isono, Y., Nagai, K. and Irie, R.
TITLE Full-length human cdna
JOURNAL Patent: EP 140981-A 1261 28-JUL-2004;
Research Association for Biotechnology (JP)
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source 1. .2374
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Best Local Similarity 87.7%; Pred. No. 2.7e-285;
Matches 1288; Conservative 0; Mismatches 6; Indels 174; Gaps 1;
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QY 1509 GCGGATTATGCAAGTCAAGTTCCAA 1536
Db 1267 GCGGATTATGCAAGTCAAGTTCCAA 1294
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AK122619 2374 bp mRNA linear PRI 09-SEP-2003
LOCUS Homo sapiens cdna FLJ16033 fis, clone SPLEN2001599, weakly similar
DEFINITION to Homo sapiens sialic acid binding immunoglobulin-like lectin 8
long splice variant (Sglec8) gene.
ACCESSION AK122619
VERSION AK122619.1 GI:34527798
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S.,
Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R.,
Otsuki, T., Sato, H., Ota, T., Wakamatsu, A., Ishii, S., Yamamoto, J.,
Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K.,
Yanashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H.,
Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K.,
Takahashi, F., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y.,
Sugano, S., Nagahara, K., Masuho, Y., Nagai, K. and Isogai, T.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished

REFERENCE

2 (bases 1 to 2374)
Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)

COMMENT

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5' & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

FEATURES

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CDS

Query Match 71.6%; Score 1100.4; DB 9; Length 2374;
Best local similarity 87.7%; Pred. No. 2.7e-285;
Matches 1288; Conservative 0; Mismatches 6; Indels 174; Gaps 1;
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RESULT 4
AX365516
LOCUS

AX365516 2565 bp DNA linear PAT 15-FEB-2002

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: WO 0168948-A 117 20-SEP-2001;
Genentech, Inc. (US)

FEATURES
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Location/Qualifiers
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ORIGIN

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RESULT 7	REFERENCE
AY358337	AUTHORS
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	

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RESULT 8
LOCUS AX365530
DEFINITION Sequence 15 from Patent WO208257.
ACCESSION AX365530
VERSION AX365530.1 GI:18697092
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Longphre, M., Chang, H. and Whitney, G.
AUTHORS Novel siglecs and uses thereof
TITLE Patent: WO 0208257-A 15 31-JAN-2002;
JOURNAL BRISTOL-MYERS SQUIBB COMPANY (US)
FEATURES Location/Qualifiers
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ORIGIN
Query Match 62.3%; Score 956.2; DB 6; Length 2208;
Best Local Similarity 73.3%; Pred. No. 2.1e-246;
Matches 1533; Conservative 0; Mismatches 3; Indels 555; Gaps 2;
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VERSION	AX365542.1 GI:18697098					
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ACCESSION      AF310233
VERSION      AF310233.1
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AUTHORS      Munday,J., Kerr,S., Ni,J., Cornish,A.L., Zhang,J.O., Nicoll,G.,
              Floyd,H., Mattei,M.-G., Moore,P., Liu,D. and Crocker,P.R.
              Identification, characterization and leucocyte expression of
              Siglec-10, a novel human sialic acid-binding receptor
              Biochem. J. 355 (Pt 2), 489-497 (2001)
JOURNAL      Biochem. J. 355 (Pt 2), 489-497 (2001)
MEDLINE      21181584
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AUTHORS      Cornish,A.L., Ni,J. and Crocker,P.R.
DIRECT SUBMISSION
TITLE      Submitted (02-OCT-2000) School of Biological Sciences, University
JOURNAL      of Dundee, Dow Street, Dundee DD6 8AT, Scotland, United Kingdom
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ORIGIN

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Query Match      62.1%; Score 954.6; DB 9; Length 2176;
Best Local Similarity 73.3%; Pred. No. 5.6e-246;
Matches 1532; Conservative 0; Mismatches 4; Indels 555; Gaps 2;

QY 1 ATGCTACTGCACTGCTGTGCTCTCGCTGTGGCGGCTCCAGGCTATGATGGAGA 60
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DB 1838 GTCCGAGCGGTGCGCCCTCTGGCTCAGAGCGGAATCAGAAAGCCACACAAACAGTCTCT 1897
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LOCUS	Sialoadhesin family 4 (SAP-4)				
DEFINITION	Sialoadhesin family 4 (SAP-4)				
ACCESSION	BD011516				
VERSION	BD011516.1	GI:18639889			
KEYWORDS	JP 2001502359-A/1.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	1. (bases 1 to 3099)				
JOURNAL	Kikly, K.K. and Miller, C.L.E.				
COMMENT	Sialoadhesin family 4 (SAP-4) cDNA				
	Patent: JP 2001502359-A 1 20-FEB-2001;				
	SMITHKLINE BEECHAM CORP				
	OS Homo sapiens (human)				
	PN JP 2001502359-A/1				
	PD 20-FEB-2001				
	PF 27-MAY-1998 JP 1999500864				
	PI KRISTINE KAY KIKLY, CONNIE LYNN ERICKSON MILLER PC				
	A61K38/00, A61K39/395, A61K48/00, C07H21/04, C07K14/435, C07K14/705, PC				
	C07K16/00,				
	PC C07K16/18, C07K16/28, C12N15/01, C12N15/11, C12N15/12, C12N15/63 CC				
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	Best Local Similarity	69.4%; Pred. No. 8.7e-201;			
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QY	61	TTCTGGATACAGTGCAGGAGTCACTGATGTCGCGGAGGCTGTGCTCTGTGCC 120			
Db	111	TTCTGGATACAGTGCAGGAGTCACTGATGTCGCGGAGGCTGTGCTCTGTGCC 170			
QY	121	TGCTCTTTCTCTACCCCGACAGGACTGGACAGGCTTACCCAGCTTATGGCTACTGG 180			
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1611	ACTCAGACAGAAACCCCGAGCCGAGTTCTCCCGGCACACGATCTCTGATTCATC 1670	Db

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1360 AAGCAGTATCAGTTGCCAGTTTCCCGAGAACCCAAATCATCCACTCAAGCCCCCAGAAATCC 1419
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DB 1957 CAGGAGAGCCAGAGGAGTCTCATTTATGCCACGCTCAACTTCCAGGGCGTCCAGACCCAGG 2016
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1
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ID AAA37847 standard; DNA; 1536 BP.
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AC AAA37847;
DT 12-FEB-2001 (first entry)
DE Human obesity protein binding protein-2 homologue coding sequence #1.
XX
KW Human obesity protein binding protein-2 homologue; hOB-BP2h; obesity;
KW obesity-related disorder; therapy; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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XX
PN WC200059942-A2.
XX
PD 12-OCT-2000.
XX
PF 22-MAR-2000; 2000WO-US006682.
XX
PR 02-APR-1999; 99US-0127667P.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Su EW, Wei J;
XX
DR WPI: 2000-664992/64.
XX
DR P-PSDB; AAY97542.
XX
PT New human obesity protein binding protein-2 homologue nucleic acids,
XX
PT polynucleotides and polypeptides useful for producing medicament for
XX
XX treating obesity and/or obesity-related disorders.
PS Claim 3; Page 85; 92pp; English.
XX
CC This sequence encodes a human obesity protein binding protein-2 homologue
CC (hOB-BP2h) of the invention. The hOB-BP2h nucleic acids and polypeptides
CC may be used for the manufacture of a medicament for the treatment of

CV 1465 GGCCTCAGACCCAGCCCTGAGCCCGGATGCCCAAGGCGACCCAGCGGATTATGCAGAA 1524
DB 1689 GGCCTCAGACCCAGCCCTGAGCCCGGATGCCCAAGGCGACCCAGCGGATTATGCAGAA 1748
CV 1525 GTCAGAGTTCCTCAA 1536
DB 1749 GTCAGAGTTCCTCAA 1760

RESULT 3
AAZ34109
TO AAZ34109 standard; cDNA; 2764 BP.
AAZ34109;
07-DEC-1999 (first entry)
DE Human PRO940 nucleotide sequence.
Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
probe; blood coagulation disorder; cancer; cellular adhesion disorder;
secreted protein; transmembrane protein; ss.
OS Homo sapiens.
PA WO9946281-A2.
DB 16-SEP-1999.
XX 08-MAR-1999; 99WO-US005028.
XX 10-MAR-1998; 98US-0077450P.
XX 11-MAR-1998; 98US-0077632P.
XX 11-MAR-1998; 98US-0077641P.
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XX 13-MAR-1998; 98US-0078004P.
XX 17-MAR-1998; 98US-00040220.
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22-MAY-1998; 98US-0086392P.
22-MAY-1998; 98US-0086414P.
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22-MAY-1998; 98US-0086486P.
28-MAY-1998; 98US-0087098P.
28-MAY-1998; 98US-0087106P.
28-MAY-1998; 98US-0087208P.
30-JUL-1998; 98US-0094651P.
11-SEP-1998; 98US-0100038P.
(GETH) GENENTECH INC.
Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
WPI; 1999-551358/46.
P-PSDB; AAY41724.
New secreted and transmembrane polypeptides and their polynucleotides,
useful for treating blood coagulation disorders, cancers and cellular
adhesion disorders.
Claim 2; Fig 92; 530pp; English.
The present invention describes secreted and transmembrane polypeptides
and their polynucleotides. The nucleotide sequences are useful as sources
of probes, primers, for chromosome mapping, and for generation of
antisense sequences. They can also be used to create transgenic animals.
The proteins can be used to treat a variety of diseases and disorders,
depending on their function. Diseases that may be treated include blood
coagulation disorders, cancers and cellular adhesion disorders. They may
also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to
AAZ41774 represent polynucleotide and polypeptide sequence given in the
exemplification of the present invention
Sequence 2764 BP; 689 A; 798 C; 717 G; 560 T; 0 U; 0 Other;

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1126 CACGAAGAGAGTTCACCTGCGAGCTCGGACCCAGCAGCTGCGCTCCGAGCAGCTCTCTC 1185
1045 AGCTCTCTCGTGCATATAGAGGAGTCTCATCTCAAGGCTCTCTCAATGAGGCTTT 1104
1186 AGCTCTCTCGTGCATATAGAGGAGTCTCATCTCAAGGCTCTCTCAATGAGGCTTT 1245
1105 CTGGGATCGGATCAGGCT 1164
1246 CTGGGATCGGATCAGGCT 1305
1165 CTACCGAAGAGAGCTCAGACAGAAACCCGAGGCGCCAGGTTCTCCCGGACAGCAGC 1224
1306 CTACCGAAGAGAGCTCAGACAGAAACCCGAGGCGCCAGGTTCTCCCGGACAGCAGC 1365
1225 ATCTGTGATACATCAATGTGTCCGAGCGCTGCGGCTGCGCTGAGTCAATCAAGATT 1284
1366 ATCTGTGATACATCAATGTGTCCGAGCGCTGCGGCTGCGCTGAGTCAATCAAGATT 1425
1285 AAAGCCACCAACAGTCTCTCGGACCCCTCTTCCAGGCTGCTCTCTCCCGGACAGCAG 1344
1426 AAAGCCACCAACAGTCTCTCGGACCCCTCTTCCAGGCTGCTCTCTCCCGGACAGCAG 1485
1345 AAGAGAACAGAAAGAGTATGATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1404
1486 AAGAGAACAGAAAGAGTATGATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1545
1405 CAAGCCAGAAATCCAGGAGCAAGAGAGCTCCATTATGCGAGCTCAACTTCCCA 1464
1546 CAAGCCAGAAATCCAGGAGCAAGAGAGCTCCATTATGCGAGCTCAACTTCCCA 1605
1465 GCGGTGAGACCCAGGCTGAGGCGCGGATGCCAAGGCGACCCAGGCGGATTTGAGAA 1524
1606 GCGGTGAGACCCAGGCTGAGGCGCGGATGCCAAGGCGACCCAGGCGGATTTGAGAA 1665
1525 GTCAGTTTCCAA 1536
1666 GTCAGTTTCCAA 1677

RESULT 7
AC89433 standard; cDNA; 2764 BP.
AC89433;
AC89433;
09-JUL-2003 (first entry)
cDNA encoding human PRO polypeptide #59.
Human; PRO polypeptide; secreted protein; transmembrane protein;
chromosome mapping; gene mapping; tumour; adrenal; lung; colon; breast;
prostate; rectal; cervical; liver; cancer; TNF-alpha;
tumour necrosis factor-alpha; proliferation; differentiation;
chondrocyte cell; bone disorder; cartilage disorder; sports injury;
arthritis; cytostatic; antiarthritic; osteopathic; gene therapy; gene;
ss.

OS Homo sapiens.
XX US2003036141-A1.
XX 20-FEB-2003.
XX 01-JUL-2002; 2002US-00187597.
XX 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059266P.
XX 17-OCT-1997; 97US-0062250P.
XX 21-OCT-1997; 97US-0063486P.
XX 24-OCT-1997; 97US-0063130P.
XX 24-OCT-1997; 97US-0083121P.
XX 28-OCT-1997; 97US-0083540P.
XX 28-OCT-1997; 97US-0063541P.
XX 28-OCT-1997; 97US-0063564P.
XX 29-OCT-1997; 97US-0063734P.
XX 31-OCT-1997; 97US-0063870P.
XX 31-OCT-1997; 97US-0084103P.
XX 13-NOV-1997; 97US-0065311P.
XX 21-NOV-1997; 97US-0066120P.
XX 24-NOV-1997; 97US-0066466P.
XX 24-NOV-1997; 97US-0066772P.
XX 11-DEC-1997; 97US-0069335P.
XX 12-DEC-1997; 97US-0069435P.
XX 17-DEC-1997; 97US-0069807P.
XX 18-DEC-1997; 97US-0068017P.
XX 10-MAR-1998; 98US-0077450P.
XX 11-MAR-1998; 98US-0077632P.
XX 11-MAR-1998; 98US-0077649P.
XX 20-MAR-1998; 98US-0078886P.
XX 20-MAR-1998; 98US-0078939P.
XX 27-MAR-1998; 98US-0079664P.
XX 27-MAR-1998; 98US-0079786P.
XX 31-MAR-1998; 98US-0080107P.
XX 31-MAR-1998; 98US-0080194P.
XX 01-APR-1998; 98US-0080327P.
XX 01-APR-1998; 98US-0080333P.
XX 08-APR-1998; 98US-0081049P.
XX 08-APR-1998; 98US-0081070P.
XX 09-APR-1998; 98US-0081195P.
XX 15-APR-1998; 98US-0081838P.
XX 21-APR-1998; 98US-0082568P.
XX 21-APR-1998; 98US-0082569P.
XX 22-APR-1998; 98US-0082704P.
XX 22-APR-1998; 98US-0082797P.
XX 28-APR-1998; 98US-0083322P.
XX 29-APR-1998; 98US-0083495P.
XX 29-APR-1998; 98US-0083496P.
XX 29-APR-1998; 98US-0083499P.
XX 29-APR-1998; 98US-0083559P.
XX 05-MAY-1998; 98US-0084366P.
XX 06-MAY-1998; 98US-0084414P.
XX 07-MAY-1998; 98US-0084633P.
XX 07-MAY-1998; 98US-0084640P.
XX 15-MAY-1998; 98US-0085579P.
XX 15-MAY-1998; 98US-0085580P.
XX 15-MAY-1998; 98US-0085582P.
XX 15-MAY-1998; 98US-0085700P.
XX 18-MAY-1998; 98US-0086023P.
XX 22-MAY-1998; 98US-0086392P.
XX 22-MAY-1998; 98US-0086486P.
XX 28-MAY-1998; 98US-0087098P.
XX 28-MAY-1998; 98US-0087208P.
XX 02-JUN-1998; 98US-0087609P.
XX 02-JUN-1998; 98US-0087759P.
XX 03-JUN-1998; 98US-0087827P.
XX 04-JUN-1998; 98US-0088025P.
XX 04-JUN-1998; 98US-0088028P.
XX 04-JUN-1998; 98US-0088029P.

466 GTGCTCAGCTTCACGCCACAGACCCAGGACCAACACACCGACCTCACCTGCGCATGTGGAC 525
460 -----CTGGAGCCGGGACGCGGTGACGGT 485
526 TTCTCCAGAAAGGTGTAGCGGCACAGAGACCGTCCGACTCGTGTGGCTATGCCGCC 585
486 CATCTGTGTGTTAACTGGGCCCTTTGAGGAATGTCCACCCCTTTCTTTCTCTGGAGGG 545
586 AGAGACCTTGTATCAGCATTTCACTGTACAAACACGCGACCTGTGAGCCCGACGCCAG 645
546 GGCTGCCCTCTCTCCCAAGGAACCAACCAACGACTCCACTTCTCAGTGTCTCAGCTT 605
646 GGAAATGTCATACCTCTGGAGGCCAAAGGCCAGTTCTGCGGTCTCTGTGTCTGTCT 705
606 CACGCCCGAGACCCGAGGACCAAC-----GACACCGACCTCAC 641
706 GACAGCCAGCCCTGCGCACACTGAGTGGTCTCTGAGAAACAGAGTCTCTCTCTGCTCC 765
642 CTGCTGTGTGACCTTCTCCAGAAAGGTGTGAGGCACACAGGACCGTCCGACTCCGTGT 701
766 CATCTCTGGGGCCCTAGACCCCTGGGCTGGAGTCCCGGGGTGAAGGTGGGGATTCA 825
702 GGCTATGTCGCCCGACAGACCTTGTATCAGCATTTTCACTGTGACAAACGCGC----- 752
826 GGGGCTACACTGCCGAGCGGAGAACAGGCTTGGCTCCGAGCGAGCGCTGTGACCTC 885
753 -----AGATCTCCAGAGAACTCAGAGTGTGTTTCCCAAGCAACACAGCAGTC 804
886 TCTGTGAGTATCTCTCCAGAGAACTCAGAGTGTGTTTCCCAAGCAACACAGCAGTC 945
805 CTGGAAGAACTTGGAAAGCGGACGCTCTCTCCAGTACTGAGGCGCAAGGCTGTGCTG 1005
946 CTGGAAGAACTTGGAAAGCGGACGCTCTCTCCAGTACTGAGGCGCAAGGCTGTGCTG 1065
865 GTCTGTGTACACACAGCAGCAGCCCGCCAGCCAGGCTGAGCTGGACCCAGAGGGGACAGTT 924
1006 GTCTGTGTACACACAGCAGCAGCCCGCCAGCCAGGCTGAGCTGGACCCAGAGGGGACAGTT 1065
925 CTGAGCCCTCCAGCCCTCAGACCCCGGGTCTCTGAGCTGCTCGGTTCAAGTGGAG 984
1066 CTGAGCCCTCCAGCCCTCAGACCCCGGGTCTCTGAGCTGCTCGGTTCAAGTGGAG 1125
985 CACGAAGAGAGTTACCTGCGACGCTCGGACCCACTGGGCTCCAGCAGCTCTCTCTC 1044
1126 CACGAAGAGAGTTACCTGCGACGCTCGGACCCACTGGGCTCCAGCAGCTCTCTCTC 1185
1045 AGCTCTCCGTGCACTATAGAGGGACTCATCTCAAGCGCATTTCTCAATGAGCGTTT 1104
1186 AGCTCTCCGTGCACTATAGAGGGAGTCACTCAAGCGCATTTCTCAAGCGCGTTT 1245
1105 CTGGAAATCGCATCACGGCTCTCTTTCTCTGCTGCGCTGATCATCATGAAGATT 1164
1246 CTGGAAATCGCATCACGGCTCTCTTTCTCTGCTGCGCTGATCATCATGAAGATT 1305
1165 CTACGAAGAGAGGACTTCAGACAGAAACCCCGAGGCGCCAGGTTCTCCCGCAGCAGC 1224
1306 CTACGAAGAGAGGACTTCAGACAGAAACCCCGAGGCGCCAGGTTCTCCCGCAGCAGC 1365
1225 ATCTGTGATTCATCAATGTGTCTCCGACGCTGCGCCCTGCTGCTCAGAGCGGAATCAG 1284
1366 ATCTGTGATTCATCAATGTGTCTCCGACGCTGCGCCCTGCTGCTCAGAGCGGAATCAG 1425
1285 AAAGCCACCAACCAAGCTCTCGGACCCCTCTTCCACAGGCTGTCTCTCCCGAGATCA 1344
1426 AAAGCCACCAACCAAGCTCTCGGACCCCTCTTCCACAGGCTGTCTCTCCCGAGATCA 1485
1345 AAGAGAGACCAAGAAAGCATATCAGTTGCGGCTGCTTCCAGAACCCAAATATCACT 1404
1486 AAGAGAGACCAAGAAAGCATATCAGTTGCGGCTGCTTCCAGAACCCAAATATCACT 1545
1405 CAAGCCCGCAGATCCAGGAGAGCCAAAGAGAGCTTCCATTATGCCAGCTCAACTTCCCA 1464
1546 CAAGCCCGCAGATCCAGGAGAGCCAAAGAGAGCTTCCATTATGCCAGCTCAACTTCCCA 1605

QY 1465 GGCTCAGACCCAGGCTGTAGGCCCGGATGCCAAGGGACCCAGGCGGATTATGCAGAA 1524
DB 1606 GGCTCAGACCCAGGCTGTAGGCCCGGATGCCAAGGGACCCAGGCGGATTATGCAGAA 1665
QY 1525 GTCAAGTTCCAA 1536
DB 1666 GTCAAGTTCCAA 1677
RESULT 8
ACA73443
ID ACA73443 standard; cDNA; 2764 BP.
XX ACA73443;
AC ACA73443;
XX
DT 01-JUL-2003 (first entry)
XX Human secreted/transmembrane protein (PRO) cDNA #59.
DE Human; ss: gene; secreted protein; transmembrane protein; PRO; tumour;
KW proliferation; differentiation; chondrocyte cells;
KW tumour necrosis factor-alpha; TNF-alpha; blood; gene therapy.
XX Homo sapiens.
XX US2003036146-A1.
XX 20-FEB-2003.
XX 02-JUL-2002; 2002US-00187603.
XX 26-JUN-1998; 98US-00105413.
PR 16-SEP-1998; 98WO-US019330.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 06-NOV-1998; 98US-00187368.
PR 01-DEC-1998; 98WO-US025108.
PR 07-DEC-1998; 98US-00202054.
PR 03-MAR-1999; 99US-00254311.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 12-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028551.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014911.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.

RESULT 9	
ACAO5758	ACA05758 standard; cDNA; 2764 BP.
ACAO5758	ACA05758;
29-MAY-2003	(first entry)
Human secreted/transmembrane protein (PRO) cDNA #59.	
Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;	
tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;	
tissue typing.	
Homo sapiens.	
US2003036162-A1.	
20-FEB-2003.	
12-JUL-2002; 2002US-00194423.	
26-JUN-1998; 98US-00105413.	
16-SEP-1998; 98WO-US019330.	
07-OCT-1998; 98US-00168978.	
07-OCT-1998; 98WO-US021141.	
06-NOV-1998; 98US-00187368.	

(GETH) GENENTECH INC.

WPI: 2003-332039/31.

WPI; 2003-332039/
P-PSDB; ABU67464.

New secreted and transmembrane PRO polypeptides and nucleic acids, useful in gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification.

XX
13

466 GTGCTCAGCTTCAGGCCAGACCCAGGACCAACACACGACCTCACCTGCTCATGTGGAC 525
460 -----CTGGAGCCCGGACGCGGTGACGGT 485
526 TTCTCCAGAAAGGTGTGACGACAGAGACCGTCCGACTCCGTGTGGGCTATGCCCC 585
486 CATCTGTGTGTTAACTGGGCTTTGAGGAATGTCACCCCTCTTTCTCTGGACGGG 545
586 AGAGACCTTGTATCAGCATTTTCAGGTGACACACGCCAGCCCTGGAGCCCAAGCCAG 645
546 GGCTGCCCTCTCTCCCAAGGAACCAACCAAGACCTCCCACTTCTCAGTGTCTAGCTT 605
646 GGAATGTCCCATCTCTGGAAGCCCAAAAGGCGAGTTCCTGGGCTCTCTGTGTGCT 705
606 CAGCCCCAGACCCAGGACCAAC-----GACACCGACCTCAC 641
706 GACAGCAGCCCTCCCACTGAGCTGGGTCTCGACAGACAGATCTCTCTCTCTGTC 765
642 CTGCCATGTGGACTTCTCCAGAAAGGTGTGACGACAGACCGTCCGACTCCGCTGT 701
766 CATCTCTGGGCTAGACCTCTGGGCTGAGCTGCCGGGTGAAGCTGGGGATTCA 825
702 GGCTATGCCCCCAGAGACCTTGTATCAGCATTTACGTGACAAACACGCC----- 752
826 GGGGCTACCTCTGCGAGCGGAGACAGCTTGGCTCCAGCAGCGAGCCCTGGACCTC 885
753 -----AGATCCTCCAGAGAACCTCAGAGTGTATGTTTCCCAAGCAACAGGACGTC 804
886 TCTGTGCAGTATCTCCAGAGAACCTCAGAGTGTATGTTTCCCAAGCAACAGGACGTC 945
805 CTGGAACCTTGGGAACGCACTCTCTCCAGTACTGGAGGGCCAAAGCTGTGCTG 864
946 CTGGAACCTTGGGAACGCACTCTCTCCAGTACTGGAGGGCCAAAGCTGTGCTG 1005
865 GTCTGTGTACACACAGCAGCCCCAGCAGCTGAGCTGGACCCAGAGGGGACAGGTT 924
1006 GTCTGTGTACACACAGCAGCCCCAGCAGCTGAGCTGAGCTGACCCAGAGGGGACAGGTT 1065
925 CTGAGCCCTTCCAGCCCTCAGACCCCGGGGCTCTGAGCTGCTCGGTTCAAGTGGAG 984
1066 CTGAGCCCTTCCAGCCCTCAGACCCCGGGGCTCTGAGCTGCTCGGTTCAAGTGGAG 1125
985 CAGAGAGGAGTTACCTGCCAGCTCGGCACCCACTGGCTCCAGACGCTCTCTC 1044
1126 CAGAGAGGAGTTACCTGCCAGCTCGGCACCCACTGGCTCCAGACGCTCTCTC 1185
1045 AGCCTCTCGTGCATATAAGAGGAGTCTATCTCAACGGCAATCTCCCAATGGAGGTTT 1104
1186 AGCCTCTCGTGCATATAAGAGGAGTCTATCTCAACGGCAATCTCCCAACGGAGGTTT 1245
1105 CTGGGATCGGATCAGGCTCTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1164
1246 CTGGGATCGGATCAGGCTCTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1305
1165 CTACCGAGAGAGGAGTCTCAGACAGAAACCCGAGGCCAGGTTCTCCCGGCACAGCAG 1224
1306 CTACCGAGAGAGGAGTCTCAGACAGAAACCCGAGGCCAGGTTCTCCCGGCACAGCAG 1365
1225 ATCTCGATTATCATTAATGTGTCGAGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 1284
1366 ATCTCGATTATCATTAATGTGTCGAGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 1425
1285 AAAGCCACACCAACAGTCTCGGACCTCTTTCCACACAGGTGCTCTCTCCCGGCAGATCA 1344
1426 AAAGCCACACCAACAGTCTCGGACCTCTCTCCACAGGTGCTCTCTCCCGGCAGATCA 1485
1345 AAGAGAACAGAAAAAGAGTATCAGTTGCCAGTTTCCAGAACCCCAATCATCCACT 1404
1486 AAGAGAACAGAAAAAGAGTATCAGTTGCCAGTTTCCAGAACCCCAATCATCCACT 1545
1405 CAGGCCCCAGATCCAGAGGAGCCAGAGGAGTCTCATTTATGCCAGCTCAACTTCCCA 1464
1546 CAGGCCCCAGATCCAGAGGAGCCAGAGGAGTCTCATTTATGCCAGCTCAACTTCCCA 1605

QY 1465 GCGCTCAGACCCAGCCCTGAGCCCGGATGCCCAAGGCAAGCCAGCGGATTATCGAGAA 1524
Db |||||
1606 GCGCTCAGACCCAGCCCTGAGCCCGGATGCCCAAGGCAAGCCAGCGGATTATCGAGAA 1665
QY 1525 GTCAGAGTTCCAA 1536
Db |||||
1666 GTCAGAGTTCCAA 1677
RESULT 11
ACF20167
ID ACF20167 standard; cDNA; 2764 BP.
XX ACP20167;
XX DT 18-SEP-2003 (first entry)
XX Human secreted polypeptide PRO940-encoding cDNA, SEQ ID NO:117.
DE KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy; gene; ss.
OS Homo sapiens.
XX US2003040063-A1.
PN 27-FEB-2003.
PD 26-JUN-2002; 2002US-00183006.
PF 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063131P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078939P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081888P.
PR 21-APR-1998; 98US-0082568P.

[illegible]

46 ATGCTACTGCCACTGCTGCTGCTCTGCTGCTGGCGGGTCCAGGCTATGGATGGAGA 105
QY 61 TTCTGATAGAGTGCAGAGTCAAGTATGGTCCGAGGGCTGTGCAATCTCTGTGCC 120
Db 106 TTCTGATAGAGTGCAGAGTCAAGTATGGTCCGAGGGCTGTGCAATCTCTGTGCC 165
QY 121 TGCTCTTTCTCTACCCCGGACAGGAGTGCAGAGGTTCTACCCAGCTTATGCTACTGG 180
Db 166 TGCTCTTTCTCTACCCCGGACAGGAGTGCAGAGGTTCTACCCAGCTTATGCTACTGG 225
QY 181 TTCAAGACAGTGAATGAGCAACCAAGGGTCTCTGTGGCCACAAACACACAGAGTGA 240
Db 226 TTCAAGACAGTGAATGAGCAACCAAGGGTCTCTGTGGCCACAAACACACAGAGTGA 285
QY 241 GAGTGAATGAGCAACCCGGGCGGATTCAGCTCACTGGGATCCCGCAGAGGGGAC 300
Db 286 GAGTGAATGAGCAACCCGGGCGGATTCAGCTCACTGGGATCCCGCAGAGGGGAC 345
QY 301 TGCTCTTTGTTGATCAGAGACGGGCGAGATGAGTCAAGTACTCTTTTCGGGTG 360
Db 346 TGCTCTTTGTTGATCAGAGACGGGCGAGATGAGTCAAGTACTCTTTTCGGGTG 405
QY 361 GAGAGGAAGCTATGAGATTAATTTTCAATGAAAGTGGTCTTTCTAAAGTAA 420
Db 406 GAGAGGAAGCTATGAGATTAATTTTCAATGAAAGTGGTCTTTCTAAAGTAA 465
QY 421 GCCTGACTCAGAGGCTGATGCTACATCCCGAGAC 459
Db 466 GTGCTAGCTTACGCCCGACACCCAGGACCAACACCGACTCACTGCGCATGTGGAC 525
QY 460 -----CTGGAGCCCGGACCGGTGACGGT 485
Db 526 TTCTCCAGAAAGGTGTGAGCGCACAGAGGACCGTCCGACTCGTGTGGCTATGCCCC 585
QY 486 CATCTGTGTTTAACTGGGCTTTGAGGAATGTCACCCCTCTCTTTCTCCTGGAGGG 545
Db 586 AGAGACCTTGTATCAGATTTCACTGTGACACACCGCAGCCCTGGAGCCCGACGCCAG 645
QY 546 GGCTGCTCTCTCTCCAGAGAACCAACCAAGAGCTCTCCACTTCTCAGTGTCTAGCTT 605
Db 646 GGAATGTCTCCATACCTGGAAGCCCAAGAGGCGAGTTCCTGGGCTCTCTGTGTGT 705
QY 606 CACGCCAGACCCCGAGACAC-----GACACCGACCTCAC 641
Db 706 GACAGACGAGCCCTCCACACTGAGCTGGGTCTCTCAGAACAGAGTCTCTCTCTGTC 765
QY 642 CTGCCATGTGAGTCTCTCAGAAAGGTGTGAGCGCACAGAGACCGTCCGACTCGTGT 701
Db 766 CATCCCTGGGCGCTAGACCCCTGGGGCTGGAGCTCCCGGGGTGAAGCTGGGATTC 825
QY 702 GGCTATGCCCCCAGAGACTTGTATACAGCAATTCACGTGACACACGCC----- 752
Db 826 GGGCGCTACACCTGCGAGCGGAGAACAGGCTTGGCTCCAGCAGCGGCCCTGGACCTC 885
QY 753 -----AGATCCTCCAGAGACCTGAGGTGATGTTTCCCAACCAACAGGACAGTC 804
Db 886 TCTGTGAGTATCTCTCAGAGAACCTGAGGTGATGTTTCCCAACCAACAGGACAGTC 945
QY 805 CTGGAACCTTTGGGACCGCAGTCTCTCCAGTACTGGAGGGCCAAAGCCTGTGCCCTG 864
Db 946 CTGGAACCTTTGGGACCGCAGTCTCTCCAGTACTGGAGGGCCAAAGCCTGTGCCCTG 1005
QY 865 GTCTGTGTACACACAGAGACCCCGCAGCGAGCTGAGCTGAGTCCAGAGGGGACAGGTT 924
Db 1006 GTCTGTGTACACACAGAGACCCCGCAGCGAGCTGAGCTGAGTCCAGAGGGGACAGGTT 1065
QY 925 CTGAGCCCTCTCCAGCCCTCAGACCCCGGGGTCTCTGAGTGGTCTCAAGTGGAG 984
Db 1066 CTGAGCCCTCTCCAGCCCTCAGACCCCGGGGTCTCTGAGTGGTCTCAAGTGGAG 1125
QY 985 CACGAAGGAGATTAACCTGCGACCGTCCGGACCCCACTGGGTCCAGACGCTCTCTCTC 1044
Db 1126 CACGAAGGAGATTAACCTGCGACCGTCCGGACCCCACTGGGTCCAGACGCTCTCTCTC 1185

QY 1045 AGCCTTCCGTGCACACTATAAGAGGAGTCACTCTCAACGGCATTTCTCAATGAGCGTTT 1104
Db 1186 AGCCTTCCGTGCACACTATAAGAGGAGTCACTCTCAACGGCATTTCTCAACGGCGTTT 1245
QY 1105 CTGGGAATGGCATCAGCGCTCTCTTTTCTCTCTGCTGGCCCTGATCATCATGAAGATT 1164
Db 1246 CTGGGAATGGCATCAGCGCTCTCTTTTCTCTCTGCTGGCCCTGATCATCATGAAGATT 1305
QY 1165 CTACCGAAGAGACGGACTCAGACAGAAACCCCGAGGCCAGGTTCTCCCGGCACAGCAG 1224
Db 1306 CTACCGAAGAGACGGACTCAGACAGAAACCCCGAGGCCAGGTTCTCCCGGCACAGCAG 1365
QY 1225 ATCTCTGGATTACATCAATGTGTGTCCTGGAGGGTGGCCCTCTGCTCAGAACGGATCAG 1284
Db 1366 ATCTCTGGATTACATCAATGTGTGTCCTGGAGGGTGGCCCTCTGCTCAGAACGGATCAG 1425
QY 1285 AAAGCCACACCAACAGTCTCTCGGACCCCTCTTCCACAGGTGCTCCCTCCCGCAATCA 1344
Db 1426 AAAGCCACACCAACAGTCTCTCGGACCCCTCTTCCACAGGTGCTCCCTCCCGCAATCA 1485
QY 1345 AAGAAGAACCGAAGAAAGCAGTATCAGTTGCCAGATTTCCAGAACCCAAATCATCTCACT 1404
Db 1486 AAGAAGAACCGAAGAAAGCAGTATCAGTTGCCAGATTTCCAGAACCCAAATCATCTCACT 1545
QY 1405 CAAGCCCCCAGATCCCGAGAGACCAAGAGGCTCCATTATGCCAGCTCAACTCCCA 1464
Db 1546 CAAGCCCCCAGATCCCGAGAGACCAAGAGGCTCCATTATGCCAGCTCAACTCCCA 1605
QY 1465 GCGCTCAGACCCAGGCTGAGGCCCGGATGCCAAGGCGACCCAGGGGATTTATGCAGAA 1524
Db 1606 GCGCTCAGACCCAGGCTGAGGCCCGGATGCCAAGGCGACCCAGGGGATTTATGCAGAA 1665
QY 1525 CTCAGTTCCAA 1536
Db 1666 GTCAAGTTCCAA 1677

RESULT 12
ACFI19553
ID ACFI19553 standard; cDNA; 2764 BP.
XX AC ACFI19553;
XX DT 17-SEP-2003 (first entry)
XX Human secreted polypeptide PRO940-encoding cDNA, SEQ ID NO:117.
DE Human; PRO; secreted protein; transmembrane protein;
XX extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy; gene; ss.
XX Homo sapiens.
XX US2003040064-A1.
PN 27-FEB-2003.
PD 27-FEB-2003.
XX 26-JUN-2002; 2002US-00183008.
PF 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 21-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0083120P.
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PR 28-OCT-1997; 97US-0063540P.
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PR 28-OCT-1997; 97US-0063544P.

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Tue Nov 9 08:29:56 2004

us-09-937-636-1.rng

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DE		PR	02-MAY-1998;	98US-0087208P.
XX		PR	02-JUN-1998;	98US-0087609P.
XX		PR	02-JUN-1998;	98US-0087759P.
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XX	tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;	PR	04-JUN-1998;	98US-0088025P.
XX	tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;	PR	04-JUN-1998;	98US-0088028P.
XX	prostate tumour; rectal tumour; cervical tumour; liver tumour.	PR	04-JUN-1998;	98US-0088029P.
XX		PR	04-JUN-1998;	98US-0088033P.
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XX	22-MAY-1998;	PR	18-AUG-1998;	98US-0097022P.

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us-09-937-636-1.rng

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1666 GTCAGTTCCAA 1677

RESULT 14

ACFI3006

ACFI3006 standard; cdna; 2764 BP.

ACFI3006;

13-SEP-2003 (first entry)

Human secreted polypeptide PRO940-encoding cdna, SEQ ID NO:117.

Human; PRO; secreted protein; transmembrane protein;
extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
Chondrocyte; proliferation; differentiation; cartilage disorder;
bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
liver; drug screening; transgenic animal; genetic analysis;
antiarthritic; vulnery; gene therapy; gene; ss.

Homo sapiens.

US2003036160-A1.

20-FEB-2003.

02-JUL-2002; 2002US-00188791.

18-SEP-1997; 97US-0059263P.
18-SEP-1997; 97US-0059266P.
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us-09-937-636-1.rng

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1525 GTCAGGTTCCAA 1536
1666 GTCAGGTTCCAA 1677

RESULT 15
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DD ACD25109 standard; cDNA; 2764 BP.

AC ACD25109;

XX ACD25109;

DT 30-AUG-2003 (first entry)

DE Human secreted/transmembrane protein (PRO) cDNA #59.

XX Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.

OS Homo sapiens.

XX US2003044925-A1.

XX 06-MAR-2003.

XX 25-JUN-2002; 2002US-00180560.

XX 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.
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Db 1666 GTCAAGTTCCAA 1677

Search completed: November 8, 2004, 09:33:12
Job time : 1075.14 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 08:08:29 ; Search time 165.477 Seconds
(without alignments)
6597.726 Million cell updates/sec

Title: US-09-937-636-1

Perfect score: 1536

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Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

Database :

- 1: /cgn2_6/prodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/prodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/prodata/1/ina/5A_COMB.seq.*
- 4: /cgn2_6/prodata/1/ina/5B_COMB.seq.*
- 5: /cgn2_6/prodata/1/ina/5A_COMB.seq.*
- 6: /cgn2_6/prodata/1/ina/5B_COMB.seq.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	364.8	23.8	1597	3	US-09-038-832-3
2	364.8	23.8	1597	3	US-09-038-832-1
3	332.4	21.6	1501	3	US-09-046-736-1
4	325.2	21.2	2027	4	US-08-896-537A-1
5	287	18.7	1488	4	US-09-620-312D-407
6	281	18.3	1437	4	US-09-023-655-1029
7	190.8	12.4	132	4	US-09-513-999C-3082
8	154.8	10.1	1502	3	US-09-046-736-3
9	153.6	10.0	231	4	US-09-513-999C-522
10	93.4	6.1	459	4	US-08-896-537A-11
C 11	39.6	2.6	505	4	US-09-621-976-15639
C 12	39.6	2.6	3132	3	US-09-286-904-45
C 13	39.6	2.6	3132	4	US-09-640-101-45
C 14	38	2.5	633	4	US-09-252-991A-1373
C 15	38	2.5	1335	4	US-09-252-991A-1196
C 16	38	2.5	1782	4	US-09-252-991A-1412
17	37.2	2.4	399	4	US-09-621-976-8976
18	37	2.4	1043	3	US-09-254-077A-5
19	37	2.4	1409	6	5242798-6
20	36.6	2.4	1478	4	US-09-148-545-63
21	36.6	2.4	1717	4	US-09-048-588-2
22	36.6	2.4	2016	4	US-09-148-545-119
23	36.4	2.4	909	4	US-09-252-991A-13406
24	36.4	2.4	942	4	US-09-252-991A-13610
C 25	36.4	2.4	1566	4	US-09-252-991A-13740
C 26	36	2.3	633	4	US-09-252-991A-11443
27	36	2.3	1355	4	US-09-252-991A-11429

C 28	36	2.3	1755	4	US-09-252-991A-11461
29	35.8	2.3	2163	1	US-07-731-157A-1
30	35.8	2.3	2163	2	US-08-541-780-1
C 31	35.4	2.3	443765	3	US-09-103-840A-2
C 32	35.4	2.3	441529	3	US-09-103-840A-1
C 33	35.2	2.3	647	4	US-09-023-655-790
C 34	35.2	2.3	2521	3	US-09-115-446-1
C 35	35.2	2.3	2521	4	US-09-565-590-1
C 36	35.2	2.3	2526	3	US-09-115-446-5
C 37	35.2	2.3	2526	4	US-09-565-590-5
C 38	35.2	2.3	7218	1	US-08-232-463-14
C 39	35.2	2.3	3529	3	US-08-141-085-3
C 40	35	2.3	255	4	US-09-016-434-197
C 41	35	2.3	909	4	US-08-016-434-185
C 42	34.8	2.3	36519	3	US-08-923-137-2
C 43	34.4	2.2	1566	4	US-09-252-991A-14361
C 44	34.4	2.2	66933	4	US-09-544-398B-11
45	34.4	2.2	66933	4	US-09-543-771-11

ALIGNMENTS

RESULT 1

US-09-038-832-3

; Sequence 3, Application US/09038832

; Patent No. 6146845

; GENERAL INFORMATION:

; APPLICANT: KIKLY, KRISTINE

; APPLICANT: ERICKSON-MILLER, CONNIE

; TITLE OF INVENTION: Sialoadhesin Family Member-2

; TITLE OF INVENTION: (SAF-2)

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA: US/09/038,832

; APPLICATION NUMBER: US/09/038,832

; FILING DATE: 11-MAR-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA: 60/041,886

; FILING DATE: 02-APR-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: PRESTIA, PAUL F

; REGISTRATION NUMBER: 23,031

; REFERENCE/DOCKET NUMBER: GH-50018

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700

; TELEFAX: 610-407-0701

; TELEX: 846169

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1597 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-09-038-832-3

Query Match 23.8%; Score 364.8; DB 3; Length 1597;

Best Local Similarity 62.1%; Pred. No. 3.1e-96;

Matches 666; Conservative 0; Mismatches 337; Indels 69; Gaps 3;

59 GATTCTCGATACGAGTGCAGGAGTCAGTGATGGTGGCGAGGGCCCTGTGCATCTCTGTGC 118
DB
277 GTTACTTGTCTGCAAGTCAGAGAGTGTGTGACGGTGCAGGAGGGCCCTGTGTCCATGTGC 336
QY 119 CCTGCTCTTCTCTTACCCCGACAGAGTGTGACAGGGTCTACCCAGCTTATGGCTACT 178
DB 337 CCTGCTCTTCTCTTACCCCGACAGAGTGTGACAGGGTCTACCCAGCTTATGGCTACT 396
QY 179 GGTTCAGAGAGTGCAGTGCAGACACCAAGGGTGTCTGTGGCCACAAACCCAGAGTC 238
DB 397 GTTTCGGGCGAGAGACAGACCATACCAAGAGGTCAGTGGCCACAAACCCAGACA 456
QY 239 GAGAGGTGGAATGAGACACCGGGGCGGATTCAGAGTCACTTGGGGATCCCGCCAAAGGGA 298
DB 457 GAGAAGTGCAGGACAGACACCGGGGCGGATTCAGAGTCACTTGGGGATCCCGCCAAAG 516
QY 299 ACTGCTCTTGGTATCAGAGACGGGAGATGCAGAGTGTGACAGTCTCTTGGGG 358
DB 517 ACTGCTCTTGGTATCAGAGACGGGAGATGCAGAGTGTGACAGTCTCTTGGGG 576
QY 359 TGGAGAGAGGAAGCT-----ATGTGAGATATAATTTTCATGAACGATGGGT 403
DB 577 TAGAGAGAGGAAGCATGAATGGAGTTACAAATCACAGTTGAATTAACAAACTAAGCAGC 636
QY 404 TCCTTTTAAAGTAACAGCCCTGACTCAGAGGCTGTGTCTACATCCCGGACCCCTGG 463
DB 637 TGTCTGTGTGTGTGACAGCCCTGACCATAGGCTGTGACATCTCTAGGACCCCTAG 696
QY 464 AGCCGGGACCGGTGACGGTCACTGTGTGTGTTAACTGGGCTTTTGAAGATGTCCAC 523
DB 697 AGTCTGGCCACTCCAGGAACCTGACTGTCTGTGGCCCTGTGAAGCAGGACAC 756
QY 524 CCCTTCTTCTCTGAGCGGGGCTGCTCTCTCTCCAGGAACCAAAACCAAGCACT 593
DB 757 CCCCCATGATCTCTGATGGGCGCTCCGCTGTCTCTCCCGGGGCCCC-----ACTACTG 810
QY 594 CCACTTCTAGTCTGAGTTCAGCGCCAGACCCAGAGCCAGACACCGACTCACT 643
DB 811 CCGGCTCTCTAGTCTGACTTACCTTACCCAAAGCCCGGAGCCAGCCAGCTCACT 870
QY 644 GCCATGTGAGTCTTCCAGAAAGGGTGTGAGCCACAGAGAACCGTCCGACTCGGTGG 703
DB 871 GTCAGGTGACCTTGCCTGGGACAGGTGTGACACAGCAGTACCGTCCGCTCGATGTGT 930
QY 704 CCTATGCCCCAGAGACCTTGTATCAGCATTTCACTGTGACACACCGCAGATCCCTCAG 763
DB 931 CCT-----ACCTCCTT 942
QY 764 AGAACCTGAGAGTGTGTTTCCCAAGCAACAGGACAGTCTCTGAAACCTTGGGAACG 823
DB 943 GGAATGTGACCATGACTGTCTTCCAGAGAGTGCACAGCATCCACAGCCTTGGGAATG 1002
QY 824 GCAGTCTCTCCAGTACTGAGGGGCGAAGCCTGTGCTGGTGTGTGTGCACACAGCA 893
DB 1003 GCTCATCTCTTTCAGTCTCTTGGGGGCGAGTCTCTGCGCCTGTGTGTCTCAACAGCA 1062
QY 894 GCCCCAGCCAGGCTGAGCTGGACCCAGAGGGGACAGATTCTCAGGCCCTTCCAGGCCCT 943
DB 1063 ATCCCTCTGCGAGCTGAGCTGACCCGGGGAGCTTACCCCTGTGCCCCCTCAGGTCT 1122
QY 944 CAGACCCCGGGTCTGTGAGTGTGCTGGGTTCAGTGTGAGGACGAAAGGAGAGTTTCACT 1003
DB 1123 CAAACCTCTGGGCTGTGAGTGTGCTGAGTGCAGCTGAGGGATGAAGGGGGAATTCACCT 1182
QY 1004 GCCAGCTGCGACCCACTGGGCTCCAGCAGCTCTCTCTCAGCTCTCTCGTGTGACTATA 1063
DB 1183 GCCAGCTCAGAGCTCAGGGCTCCCGAGCAGCATTTCCCTGAGCTCTCTCTGAGATG 1242
QY 1064 AGAAGGAGCTCATCTCAACGGCATTTCTCAATGGAGGCTTTCTGGGAATCGG 1115
DB 1243 AGGGCAGAGGACCTCTAAGACCTGTATCACAAGTGACACTGGCAGCAGTGG 1294

RESULT 2
US-09-038-832-1
; Sequence 1, Application US/09038832
; Patent No. 6146845
; GENERAL INFORMATION:
; APPLICANT: KIRLY, KRISTINE
; APPLICANT: ERICKSON-MILLER, CONNIE
; TITLE OF INVENTION: Stalodhesin Family Member-2
; TITLE OF INVENTION: (SAP-2)
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,832
; FILING DATE: 11-MAR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/041,886
; FILING DATE: 02-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2900 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-038-832-1

Query Match 23.8%; Score 364.8; DB 3; Length 2900;

Best Local Similarity 52.1%; Pred. No. 4.1e-96; Mismatches 337; Indels 59; Gaps 3;
Matches 666; Conservative 0;

QY 59 GATTCTGTGATAGCAGTGCAGGAGTCACTGTGGTCCCGAGGGCCCTGTGCATCTCTGTGC 118
DB 137 GTTACTTGTCTGCAAGTGCAGGAGTGTGTGACGGTGCAGGAGGGCCCTGTGTCCATGTGC 196
QY 119 CCTGCTCTTCTCTTACCCCGACAGAGTGTGACAGGGTCTACCCAGCTTATGGCTACT 178
DB 197 CCTGCTCTTCTCTTACCCCGACAGAGTGTGACAGGGTCTACCCAGCTTATGGCTACT 256
QY 179 GGTTCAGAGAGTGCAGTGCAGACACCAAGGGTGTCTGTGGCCACAAACCCAGAGTC 238
DB 257 GTTTCGGGCGAGAGACAGACCATACCAAGAGCTTCCAGTGGCCACAAACCCAGACA 316
QY 239 GAGAGGTGGAATGAGACACCGGGGCGGATTCAGAGTCACTTGGGGATCCCGCCAAAGGGA 298
DB 317 GAGAAGTGCAGGACAGACACCGGGGCGGATTCAGAGTCACTTGGGGATTCAGAGCAAG 376
QY 299 ACTGCTCTTGGTATCAGAGACGGGAGATGCAGAGTGTGACAGTCTCTTCTTGGG 358
DB 377 ACTGCTCTTGGTATCAGAGACGGGAGATGCAGAGTGTGACAGTCTCTTCTTGGG 436
QY 359 TGGAGAGAGGAAGCT-----ATGTGAGATATAATTTTCATGAACGATGGGT 403
DB 437 TAGAGAGAGGAAGCATGAATGGAGTTACAAATCACAGTTGAATTAACAAACTAAGCAGC 496

404 TCTTTCTAAAGTAACAGCCCTGACTCAGAGCCTGATGCTATACATCCCGAGACCCCTGG 463
497 TGCTGTGTTGTGACAGCCCTGACCATAGGCTGACATCTCTATCTCTAGGACCCCTAG 556
464 AGCCCGGACCGGTGACGGTCTATCTGTGTTAACTGGGCTTTGAGGAATGCCAC 523
557 AGTCTGCCACTCAGGAACCTGACCTGCTCTGTGCCCTGGGCTGTAAAGCAGGGACAC 616
524 CCCTCTTTCTCTGAGCGGGGCTGCCCTCTCTCTCCCAAGGAACCAACCAACGACCT 583
617 CCCCATGATCTCTGGATTGGGCTCGCTGTCTCCCGGGCCCC-----ACTACTG 670
584 CCACCTCTCAGTCTCAGCTTACGCCAGACCCAGGACCCAGGACCCGACCTCACCT 643
671 CCGCTCTCAGTCTCAGCTTACGCCAGACCCAGGACCCAGGACCCGACCTCACCT 730
644 GCATGTGGACTCTCCAGAAAGGTGTAGCGGCACAGAGGACCCGCTCCGACTCCGTGTGG 703
731 GTGAGTGACCTTGCCTGGACAGGTGTGACACGACCACTAGCTCGCTCGCTCGATGTGT 790
704 CTTATGCCCCAGAGACCTTGTATCAGCATTTTCACTGTGACAAACAGCCAGATCTCCAG 763
791 CCT-----ACCTCCTT 802
764 AGAACCTGAGAGTATGTTTCCCAAGCAAAAGGACAGTCTCTGGAAACCTTTGGGAACG 823
803 GGAACCTGACATGATCTTCAAGGAGATGCCAGATCCACAGCCCTGGGAATG 862
824 GCAGCTCTCCAGTACTGAGGGGCAAAAGCTGTGCTCTGCTGTGTGTACACACAGCA 883
863 GCTCATCTTTCAGTCTTTCAGTCTTTCAGTCTTTCAGTCTTTCAGTCTTTCAGTCT 922
884 GCGCCCGACGAGCTGAGCTGACCCAGAGGGGACAGGTCTCTGAGCCCTCCAGCCCT 943
923 ATCCCCCTGACGCTGAGCTGACCCCGGGGAGCTGACCCCTGTCGCCCTCAGGTCTCT 982
944 CAGACCCCGGGGCTCTGAGCTGCTCGGCTTCAAGTGGAGCAGGAGGAGTTCACCT 1003
983 CAACCTCTGGCTCTGAGCTGCTCGAGTGCAGCTGAGGAGTGAAGGGGATTCACCT 1042
1004 GCACGCTCGGACCCCTAGCTGGCTCCAGCAGCTCTCTCTCAGCTCTCTCGGTGCACTATA 1063
1043 GCGAGCTCAGAGCTCAGGGCTCCAGCAGCATTTCCCTGAGCTCTCCCTGAGAAATG 1102
1064 AGAAGGACTCATCTCAACGGCTTCCAAATGAGGCTTCTTGGGAATCGG 1115
1103 AGGCACAGGACCTCAAGACCTGTATCACAAGTGACACTGGCAGCAGTCCG 1154

RESULT 3

US-09-046-736-1

Sequence 1, Application US/09046736

Patent No. 6090582

GENERAL INFORMATION:

APPLICANT: KIRBY, KRISTINE

APPLICANT: ERIKSON-MILLER, CONNIE

TITLE OF INVENTION: Sialoadhesin Family Member-3

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ratner & Prestia

STREET: P.O. Box 980

CITY: Valley Forge

STATE: PA

COUNTRY: USA

ZIP: 19482

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/046,736

FILING DATE: 24-MAR-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/041,885
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-50019
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1501 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-046-736-1

Query Match 21.6%; Score 332.4; DB 3; Length 1501;
Best Local Similarity 60.7%; Pred. No. 8.4e-87;
Matches 671; Conservative 0; Mismatches 366; Indels 69; Gaps 5;

QY 61 TTCTGATACGATGTCAGAGTCTCAGTATGTTGCGGAGGCGCTGTGATCTCTCTGCCC 120
Db 98 TACTCGCTGAGATCAGAGTTCCTGTACCGTGCAGAGGGCATGTGTCCATGTGCGC 157
QY 121 TGCTCTTTCTCCTACCCCGACAGGACTGGAAGGGTCTACCCAGCTTATGGCTACTGG 180
Db 158 TGCTCTTTCTCCTACCCAGTGGACAGCCAGACTGACTCTGACCCAGTTCATGGCTACTGG 217
QY 181 TTCAAAGCAGTGTGACAGCAACCAAGGGTCTCTGTGGCCACAAACCCAGAGTCTGA 240
Db 218 TTCGGGCGAGGAATGATATAGCTGGAAGGCTCAGTGGCCCAACAACCCAGCTTGG 277
QY 241 GAGGTGGAATAGACACCCCGGGCGGATTCAGCTCACTGGGGATCCCGCCAAAGGGGAA 300
Db 278 GCAGTGCAGGAGGAACCTCGGGACCGATTCCACCTCTCTGGGACCCACAGACCAAAAT 337
QY 301 TGCTCTTTGTTGATCAGAGACCGGAGATGAGGATGAGTACAGTACTTCTTCGGGTG 360
Db 338 TGACCCCTGAGCATCAGAGATGCCAAGATGATGCGGGAGATCTTCTTCGTATG 397
QY 361 GAGAGAGGAAGCTATGTGAGATATAATTTCAATGACAGATGGTCTCTTCTAAAGTAACA 420
Db 398 GAGAAAGGAA---ATATAAATGGAAATTAATAATATGACCACTCTCTGTGACGTGACA 454
QY 421 GCCCTGACTCAGAGCCTGATGTCTATATCCCGAGACCCCTGGAGCCCGGGCAGCCGGTG 480
Db 455 GCCTTGACCCACAGGCCCAACATCCTTATCCCGGTACCTGGAGTCTGGCTTCCAG 514
QY 481 ACGGTCACTGTGTGTTTAACTGGGCTTTGAGGAATGTCACACCCCTCTTCTCTCTGG 540
Db 515 AATCTGACCTGTCTGTGCCCTGGGCTGTGAGCAGGGAGCGCCCCCTATGATCTCTCTGG 574
QY 541 ACGGGGGTGGCCCTCTCTCTCCCAAGGAACCAACCAAGACTTCCACTTCTCAGTGTCT 600
Db 575 ATGGGGACCTGTGTCTCCCTCC-----CGCACCCCTCCACCAACCCGCTCTCTCGGTGCTC 628
QY 601 AGCTTCAGCCCGACAGCCCGCAGGACCCAGACCCGACCTCAGCTGCAATGTGACTTCTCC 660
Db 629 ACCCTCATCCCAAGCCCGCAGCACCGACCCAGCCTCAGCTGTCAAGTACCTTGGCT 688
QY 661 AGAAAGGGTGTGAGCGGCACAGAGGACCGTCCGACTCTCCGTGTGGCCCTATGCCCCCAGAGAC 720
Db 689 GGGGCGGCGGTGACCAAGGACCATCCAACTCATGTCTCTCTAC-----736
QY 721 CTGTGTATCAGCATTTACGTGACAAACAGCCAGATCTCCAGAGAACTGTGAGATGATG 780
Db 737 -----CCTCCTCAGAACTGTGACTGTGACT 760

APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing-A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yungqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 656962el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt FL_genes Version 1.0
SEQ ID NO 407
LENGTH: 1488
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (146)..(931)
US-09-620-312D-407

Query Match 18.7%; Score 287; DB 4; Length 1488;

Best Local Similarity 66.0%; Pred. No. 1.4e-73;
Matches 465; Conservative 0; Mismatches 230; Indels 10; Gaps 3;

QY 2 TGCTACTGCCACTGCTCTCTCGCTGCTGGGCGGGTCCAGGCTATGGATGGAGAT 61
DB 76 TCGCGTGTGCTGCGCTCCCTCTGCTG-TGGCAGGCGCTCGCTCAGATGCAAGAT 134
QY 62 TCTGGATACAGATGACAGATGATGATGTCGGAGGCGCTGTGCACTCTGTGCGCT 121
DB 135 TCCGGCTGGAGATGCCAGATCGGTGACGGTGCAGGAGGCTGTGTCATCTTTGTGCACT 194
QY 122 GCTCTTTCTCTACCCCGACAGACTGGACAGGCTACCCAGCTTATGGTACTGCT 181
DB 195 GTTCGGTTCTACTCGATATGGCTGGAAGATCTACCCCTGCTTATGGCCACTGGT 254
QY 182 TCAAAGCAGTGACTGAGACCAACCAAGGCTCTCTGTGGCCACAAACCAACAGATCGAG 241
DB 255 TCCGGGAAGGGTCAGTGTAGACAGGAGACTCCAGTGGCCACAAACCAACTCAACTCAA 314
QY 242 AGTGGAAATGAGACCCGGGGCGGATTCAGCTCACTGGGATCCGCCAAGGGAAC 301
DB 315 AAGTGCAGAGAGGAGACCCAGGGCGGATTCACCTCTCGGTGATCCCTCAAGGAACA 374
QY 302 GCTCTTTGTGATCAGAGACCGCAGATGATGAGATGATGATGATGATGATGATGATG 361
DB 375 GCTCCCTGACATCAGAGACCGCAGAGAGGAGGACACGGTTCATCTCTTTTGGGTG 434
QY 362 AGAGAGAACTATGATGATATATTTCTATGACAGATGGTCTTTCTAAAGTAACAG 421
DB 435 CGAGAGGAAG---AACAAATTTAGTTACAAATATTTCCCGCTCTCTGTGTATGTGACAG 491
QY 422 CCCTGACTCAGAGCTGATGTTTACATCCCGAGACCTTGGAGCCCGGCGAGCGGTGA 481
DB 492 CCCTGACCCAGCGCCGACATCTCTATCCCGAGTTCTTAAAGTGTGCGCATCCAGCA 551
QY 482 CGGTCACTGTGTTTAACTGGGCTTTGAGGAATGTCACCCCTTTCTCTCTGGA 541

DB 552 ACCTGACCTGCTCTGTGCGCTGGGTCTGTGACGAGGACACCCCATCTTCTCTGGA 611
QY 542 CGGGGCTGCTCTCTCTCCCAAGGAACAAACCAAGCACTTCCCACTTCTCAGTGCTCA 601
DB 612 TGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 665
QY 602 GCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 661
DB 666 CGATCATCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 725
QY 662 GAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 706
DB 726 GAGCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770

RESULT 6

US-09-023-655-1029
Sequence 1029, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HERewith
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1029:
SEQUENCE CHARACTERISTICS:
LENGTH: 1437 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: gl80097
US-09-023-655-1029

Query Match 18.3%; Score 281; DB 4; Length 1437;

Best Local Similarity 61.8%; Pred. No. 8e-72;
Matches 484; Conservative 0; Mismatches 290; Indels 9; Gaps 2;

QY 1 ATGCTACTGCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
DB 13 ATGCGCGTGTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 72
QY 61 TTCTGGATACGAGTGCAGGAGTCACTGATGTGTCGGAGGCGCTGTGATCTCTGTGCCC 120

DB 73 TTCTGGCTGCAAGTGCAGGAGTCTAGTACGCTACAGGAGGTTTGTGCGTCTCGTGGCC 132
QY 121 TGCTTTCTCTCTCCCGGACAGGACTGGACAGGCTTACCCAGGCTTATGGCTACTGG 180
DB 133 TGCATTTCTTCCATCCCATCTACTACGACAGAACTCCCGAGTTCTGGTACTGG 192
QY 181 TTCAAAGCAGTGTGACAGAACCAAGGGTCTCTGTGGCCCAAAACCAACCCAGAGTCGA 240
DB 193 TTCGGGAAGGAGGCAATATATCCGGGAGCTCTCCAGTGGCCCAAAACAAGCTAGATCAA 252
QY 241 GAGGTGGAATGAGCACCGGGGCGGATCCAGCTCACTGGGATCCGCAAGGGGAAC 300
DB 253 GAAGTACAGGAGGAGACTCGAGGAGATTCGGCTCTTGGGATCCAGTAGGAACAAC 312
QY 301 TGCTCTTGGTGATCAGAGACGCGCAGATGCGAGTACAGTACTTCTTTCGGGTG 360
DB 313 TGCTCCCTGAGCATCGTAGACGCCAGGAGGAGGATAATGTTTCATATCTTCTTCGGATG 372
QY 361 GAGAGAGGAGCTATGTGAGATATAATTTATGACGATGGTTCTTCTAAAGTAACA 420
DB 373 GAGAGAGGAAG---TACCAATACAGTTACAAATCTCCCGAGCTCTCTGTGCAATGACA 429
QY 421 GCCCTGACTCAGAAAGCTGTGTCTATATCCCGAGACCTCGGAGCCCGGCGAGCGGTG 480
DB 430 GACTTGACCCACAGGCCCAAAATCTCATCTCTGCACTCTAGAACCCGCGCACTCCAAA 489
QY 481 ACGGTCTCTGTGTGTTAACTGGGCTTTGAGGAATGTCCACCCCTTCTTCTCTGG 540
DB 490 AACCTTACTCTCTGTGTCTGCGCTGTGAGCAGGAAACACCCCGATCTTCTCTCTGG 549
QY 541 ACGGGGTGCTCTCTCTCCCAAGGAACCAAAACCAAGCACTCCCACTTCTCAGTCTC 600
DB 550 TTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 603
QY 601 AGCTTACGCGCCAGACCCAGGACACGACACCAACCACTCACTGCTGCTGCTGCTGCTGCT 660
DB 604 ATAATCACCCACGCGCCAGGACACGACACCAACCACTCACTGCTGCTGCTGCTGCTGCT 663
QY 661 AGAAGGAGTGTGAGGACACGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 664 GGAGCTGTGTGACTACGAGAGACACATCCAGCTCAAGCTACATGTTCCACAGAAC 723
QY 721 CTGTTATCAGCATTTCACTGACACACGACGACATCTCCAGAGAACCTGAGAGTGTG 780
DB 724 CCAACAATGTTATCTTCCAGGAGATGGCTCAGGGAACCAAGAGACGAGCAGGAGTGT 783
QY 781 GTT 783
DB 784 GTT 786

RESULT 7
US-09-513-999C-3082
; Sequence 3082, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 3082
; LENGTH: 192
; TYPE: DNA
; ORGANISM: Homo sapiens

FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..192
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 12
; OTHER INFORMATION: s-g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 84
; OTHER INFORMATION: s-g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 105
; OTHER INFORMATION: s-g or c
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 28
; OTHER INFORMATION: xaa=His or Gln
; US-09-513-999C-3082

Query Match 12.4%; Score 190.8; DB 4; Length 192;
Best Local Similarity 98.4%; Pred. No. 66-45; 0; Indels 0; Gaps 0;
Matches 189; Conservative 3; Mismatches 0

QY 391 ATGAACGATGGGTTCTTTCTTAAAGTAACAGCCCTGACTCAGAACCTGATGTCTACATC 450
DB 1 ATGAACGATGGGTTCTTTCTTAAAGTAACAGCCCTGACTCAGAACCTGATGTCTACATC 60
QY 451 CCGGAGACCTCGAGCCCGGGCAGCCGGTACGCTCATCTGTGTGTTAACTGGGCTTT 510
DB 61 CCGGAGACCTCGAGCCCGGGCAGCCGGTACGCTCATCTGTGTGTTAACTGGGCTTT 120
QY 511 GAGGATGTCCACCCCTTCTTTCTCTGGAGCGGGGCTGCCCTCTCTCCCAAGGAACC 570
DB 121 GAGGATGTCCACCCCTTCTTTCTCTGGAGCGGGGCTGCCCTCTCTCCCAAGGAACC 180
QY 571 AAACCAAGGACC 582
DB 181 AAACCAAGGACC 192

RESULT 8
US-09-046-736-3
; Sequence 3, Application US/09046736
; Patent No. 6090582
; GENERAL INFORMATION:
; APPLICANT: KIKLY, KRISTINE
; APPLICANT: ERICKSON-MILLER, CONNIE
; TITLE OF INVENTION: Sialoadhesin Family Member-3
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,736
; FILING DATE: 24-MAR-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/041,885
; FILING DATE: 02-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031


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; REFERENCE/DOCKET NUMBER: GH-50019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1502 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-046-736-3

Query Match      10.1%; Score 154.8; DB 3; Length 1502;
Best Local Similarity 63.8%; Pred. No. 5.2e-35;
Matches 272; Conservative 0; Mismatches 142; Indels 12; Gaps 2;

QY 741 TGACAAACCCAGATCTCCAGAGAACCTGAGAGTATGGTTCCCAAGCAACAGGAC 800
Db      |||
QY 497 TGTGAACGTGACATACCTCTCAGAACTTGACTGTCTTCCAAGGAGAAGGCAC 556
Db      |||
QY 801 AGTCCTGMAAACCTTGGGAACGCGACGTCTCTCCAGTACTGGAGGCCAAAGCCTGTG 860
Db      |||
QY 557 AGATCCACAGCTCTGGGGAACAGCTCATCTCTTTCAGTCTCTAGAGGGCCAGTCTCTGG 616
Db      |||
QY 861 CCTGGTCTGTGTACACACAGACGACCCGCCAGCAGCTGAGCTGGACCCAGAGGGGACA 920
Db      |||
QY 617 CTGGTCTGTGTGTACACAGCAATCCCTCTGCGAGCTGAGCTGGACCTGGAGGAGTCT 676
Db      |||
QY 921 GGTCTGAGCCCTCCAGCCCTCAGACCCCGGGGCTCTGGAGCTGCTGGTTCAAGT 980
Db      |||
QY 677 GACCTGTACCCCTCAGCCCTCAACCCCTCTGGTACTGGAGCTG---CAAGTGCACCT 733
Db      |||
QY 981 GGAGCACAAAGGAGTTACCTTGCACGCTCGGCACCCACTGGGTCCAGCACCTCTC 1040
Db      |||
QY 734 GGGGATGAGGGGAATTACCTGTGAGCTGAGAATCTCTGGGTTCCAGCACCTTTC 793
Db      |||
QY 1041 TCTAGCCTCTCGTGACATATAGAGGAGCTCA-----TCTAACGGCATCTC 1091
Db      |||
QY 794 CTTGAACCTCTCCCTGCAACAGAGTACACAGGCAAAATGAGGCCCTGTATCAGGAGTGT 853
Db      |||
QY 1092 CAATGAGCGTTTCTGGGATCGCATCAGGCTCTCTTTCTCTGCTGCGCCCTGAT 1151
Db      |||
QY 854 GCTGGGGCGGTGGGGGAGCTGGACCAAGCCCTGTCTTCTCTCTCTCTCTCTCTCT 913
Db      |||
QY 1152 CATCAT 1157
Db      |||
QY 914 CTTCAT 919
Db      |||

RESULT 9
US-09-513-999C-522
; Sequence 522, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 522
; LENGTH: 231
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: May be any nucleotide
; NAME/KEY: misc_feature
; LOCATION: (26)..(26)
; OTHER INFORMATION: May be any nucleotide
; NAME/KEY: misc_feature
; LOCATION: (161)..(161)
; OTHER INFORMATION: May be any nucleotide
; NAME/KEY: misc_feature
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; NAME/KEY: CDS
; LOCATION: 62..229
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 62..109
; OTHER INFORMATION: score 11.3
; OTHER INFORMATION: seq PLLSSLLGGQA/MD
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 85
; OTHER INFORMATION: m=a or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 178
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 179
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 24
; OTHER INFORMATION: Xaa=Ala or Ser
; US-09-513-999C-522

Query Match      10.0%; Score 153.6; DB 4; Length 231;
Best Local Similarity 97.6%; Pred. No. 4.6e-35;
Matches 164; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 ATGCTACTGCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
Db      |||
QY 62 ATGCTACTGCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 121
Db      |||
QY 61 TTCTGATACAGTGCAGGAGTCACTGATGTCGCGAGGCGCTTGTGATCTCTCT-GCC 119
Db      |||
QY 122 TTCTGATACAGTGCAGGAGTCACTGATGTCGCGAGGCGCTTGTGATCTCTCTGTC 181
Db      |||
QY 120 CTGCTCTTTCTCTACCCCGACAGGACTGGACAGGCTTACCCAGC 167
Db      |||
QY 182 CTGCTCTTTCTCTACCCCGACAGGACTGGACAGGCTTACCCAGC 229
Db      |||

RESULT 10
US-08-896-537A-11
; Sequence 11, Application US/08896537A
; Patent No. 6590088
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: CD33-Like Protein
; FILE REFERENCE: 1488.9480001
; CURRENT APPLICATION NUMBER: US/08/896,537A
; CURRENT FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 60/022,481
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 11
; LENGTH: 459
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: May be any nucleotide
; NAME/KEY: misc_feature
; LOCATION: (26)..(26)
; OTHER INFORMATION: May be any nucleotide
; NAME/KEY: misc_feature
; LOCATION: (161)..(161)
; OTHER INFORMATION: May be any nucleotide
; NAME/KEY: misc_feature
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LOCATION: (310)..(310)
OTHER INFORMATION: May be any nucleotide
NAME/KEY: misc feature
LOCATION: (325)..(325)
OTHER INFORMATION: May be any nucleotide
NAME/KEY: misc feature
LOCATION: (328)..(328)
OTHER INFORMATION: May be any nucleotide
NAME/KEY: misc feature
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NAME/KEY: misc feature
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LOCATION: (349)..(349)
OTHER INFORMATION: May be any nucleotide
NAME/KEY: misc feature
LOCATION: (376)..(376)
OTHER INFORMATION: May be any nucleotide
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LOCATION: (388)..(388)
OTHER INFORMATION: May be any nucleotide
NAME/KEY: misc feature
LOCATION: (392)..(392)
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LOCATION: (415)..(415)
OTHER INFORMATION: May be any nucleotide
NAME/KEY: misc feature
LOCATION: (419)..(419)
OTHER INFORMATION: May be any nucleotide
NAME/KEY: misc feature
LOCATION: (421)..(421)
OTHER INFORMATION: May be any nucleotide
NAME/KEY: misc feature
LOCATION: (428)..(428)
OTHER INFORMATION: May be any nucleotide
NAME/KEY: misc feature
LOCATION: (434)..(434)
OTHER INFORMATION: May be any nucleotide
NAME/KEY: misc feature
LOCATION: (436)..(436)
OTHER INFORMATION: May be any nucleotide
NAME/KEY: misc feature
LOCATION: (438)..(438)
OTHER INFORMATION: May be any nucleotide
NAME/KEY: misc feature
LOCATION: (442)..(442)
OTHER INFORMATION: May be any nucleotide
NAME/KEY: misc feature
LOCATION: (445)..(445)
OTHER INFORMATION: May be any nucleotide
NAME/KEY: misc feature
LOCATION: (449)..(449)
OTHER INFORMATION: May be any nucleotide
NAME/KEY: misc feature
LOCATION: (459)..(459)

OTHER INFORMATION: May be any nucleotide
US-08-896-537A-11

Query Match 6.1%; Score 93.4; DB 4; Length 459;
Best Local Similarity 58.6%; Pred. No. 2.3e-17;
Matches 177; Conservative 0; Mismatches 124; Indels 1; Gaps 1;
QY 171 TGGCTACTGGTTCAAAGCAGTCTGAGACAAACCAAGGGTCTCTCTGGGCCAACAACCA 230
DB 4 TCGGCANAGGTTCCGGGACGGGNAGATCCCATACTACCTGAGGTGTGGCCCAACAACA 63
QY 231 CCAGAGTCGAGAGGTGGAAATGAGCACCCGGGGCGGATTCAGAGTCTCACTGGGGATCCGC 290
DB 64 CCCAGACAGAGAGTGAAGCCAGAGACCCAGGGCGGATTCCTCTGGGGATGTCCA 123
QY 291 CAAGGGAACTGCTCTTGGTGATCAGAGAGCGGAGATGAGAGATGATGACAGTACACTT 350
DB 124 GAAGAAGAACTGCTCTCTGAGATCGGAGATCCAGAAATGAGAGACAGCGGAAGCTATT 183
QY 351 CTTTCGGGTGGAGAGAGGAAGCTATGT-GAGATATAATTTTCATGAACGATGGTTCCTTC 409
DB 184 CTTCCGGGTGGAGAGAGGAAGGATGTAAATAATATAGCTACACAGATAAGCTGAAT 243
QY 410 TAAAGTAAAGCCCTGACTCAGAAAGCCTGATGTCTACATCCCGAGACCTCGGAGCCG 469
DB 244 TGGAGGTGACAGCCCTGATAGAGAAACCCGACATCCACTTTTGGAGCCTTTGGAGTTC 303
QY 470 GG 471
DB 304 GG 305

RESULT 11

US-09-621-976-15639/c
Sequence 15639, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 15639
LENGTH: 505
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-15639

Query Match 2.6%; Score 39.6; DB 4; Length 505;
Best Local Similarity 11.2%; Pred. No. 0.12;
Matches 42; Conservative 165; Mismatches 169; Indels 0; Gaps 0;
QY 272 AGCTACTGGGGATCCCGCAAGGGAAGTCTCTCTGGTGATCAGAGACGGCAGATGC 331
DB 397 RGMRCARGTGSWSKGGYRMWGRMAAAKMRMAAAGSYCGMTSVTSCKMTGRKGS 338
QY 332 AGGATGAGTCACAGTACTTTCTTCGGGTGGAGAGGAAGCTATGTGAGATATAATTCA 391
DB 337 MTKRKEMTYSGMWTSYKCTKTGKKYTKWSKKTRWCTSWRKYMMWMSGWARSMKSW 278
QY 392 TGAACGATGGGTCTTTCTTAAAGTAAACAGCCCTGACTCAGAACCTGATCTACATCC 451
DB 277 ARSWYMMVACWCMMSASAYRARRSMYARRRAGAGWARRRKKRARRKRSKMSRSM 218
QY 452 CGAGACCTCGAGCCCGGAGCGGTGACGGTCACTGTGTGTAACTGGGCGCTTTG 511
DB 217 SSMRMSAGKAFMCRWMSCRMYSYCMGSKMCRGTCAKMWRYARVAKRYASSMGKYM 158
QY 512 AGGAATGTCACCCCTCTTTCTCTGGACGGGGGTGGCCCTCTCTCCCAAGAACA 571

Tue Nov 9 08:29:56 2004

us-09-937-636-1.rni

1078	TCACGCGATTCTCCAAATCGAGCGTTCTTCGGGAATCGGCATCAGGCTCTCTCTTTCCCTC	1137
DB		
386	GTACCGCGGTGGCGCTGGGAAGCGGTATGTCCACGACACCTGGAGCTGGTCTACGAC	445
DB		
1138	TGCTGGGCC	1147
DB		
446	CGCCTGGGCGC	455
DB		

RESULT 15

RESULTS
US-09-252-991A-1196/c

US=09-252-331A-1138/C
: Sequence 1196, Application US/09252991A

; Sequence 1136, App
Patent No. 6551795

GENERAL INFORMATION:

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.

APPLICANT: MARC J. RUBENFELD et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELAT-
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSIS
FILE REFERENCE: 107196.136

FILE REFERENCE: 107196:136
CURRENT APPLICATION NUMBER: US/09

US/09/252,395

CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074-788

PRIOR APPLICATION NUMBER: US 60/014,188
PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/131,111

PRIOR APPLICATION NUMBER: UT
PRIOR FILING DATE: 1998-07-23

PRIOR FILING I
NUMBER OF SEC

NUMBER OF SEQ
SEQ ID NO 1196

SEQ	ID	NO
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98	98	98
99	99	99
100	100	100

LENGTH: 1335
TYPE: DNA

TYPE: DNA
ORGANISM: Bacillus

ORGANISM: *Pseudomonas aeruginosa*
 US-09-252-991A-1196
 Query Match 2.5% Score 38; DB 4; Length 1335;
 Best Local Similarity 45.2%; Pred. No. 0.57;
 Matches 140; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

[illegible]

Search completed: November 8, 2004, 20:38:22
Job time : 173.477 secs

PRIOR APPLICATION NUMBER: 60/081817	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081938	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568	PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569	PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796	PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336	PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322	PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742	PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366	PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414	PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441	PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582	PRIOR FILING DATE: 1998-05-13

PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085700
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085689
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085580
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 70.2%; Score 1078.8; DB 9; Length 2764;
Best Local Similarity 81.4%; Pred. No. 0;
Matches 1329: Conservative 0; Mismatches 207; Indels 96; Caps 3;

QY	1	ATGCTACTGCAC	TGCTGCTCTCTCCTCCTCTGCTGGCGGGTCCCAAGGCTATGSGATGGGAGA	60
DB	46	ATGCTACTGCAC	TGCTGCTCTCCTCCTCTGCTGGCGGGTCCCAAGGCTATGSGATGGGAGA	105
QY	61	TTCTGGATACGAG	TGCAGGAGTCAGTCATGGTGGCGGAGGCGCTGTGCATCTCTGTGCC	120
DB	106	TTCTGGATACGAG	TGCAGGAGTCAGTCATGGTGGCGGAGGCGCTGTGCATCTCTGTGCC	165
QY	121	TGCTCTTTCTC	TACCCCGACAGGACTGGACAGGGTCTACCCAGGCTTATGCTACTGG	180
DB	166	TGCTCTTTCTC	TACCCCGACAGGACTGGACAGGGTCTACCCAGGCTTATGCTACTGG	225
QY	181	TTCAAAACAGT	GACTGAGACAAACAAAGGTGCTCTCTGGGCCACAAACACCAAGAGTCGA	240
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DB	586	AGAGACCT	TGTTATTCAGCATTTTCAGTGTACAAACACGCGCGCTTGGAGCCCGACCGCCAG	645
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QY	642	CTGCCATGT	GGACATCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGT	701
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RESULT 3
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US-09-978-697-258, Application US/03978697
: Sequence 258,
: Patent No. US20020163284A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnovers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang

```

APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PLC27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918595
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742

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DB 1246 CTGGGATCGGCATCAGGCTCTCTTTCTCTGCTGGCTGGCTGATCATCATGAGATT 1305
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DB 1306 CTACCGAAGAGCGGACTCAGACAGAAACCCGAGGCCAGGTTCTCCCGGCACACAGCG 1365
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QY 1525 GTCAAGTTCCAA 1536
DB 1666 GTCAAGTTCCAA 1677

RESULT 5

US-09-999-832A-258
; Sequence 258, Application US/09999832A
; Publication No. US20020192706A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630FIC63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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24	PRIOR FILING DATE: 1998-05-07
25	PRIOR APPLICATION NUMBER: 60/084598
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53	PRIOR APPLICATION NUMBER: 60/085697

Matches 1329: Conservative 0: Mismatches

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46	ATGCTACTGCCACTGCTGTCTCTCGCTGCTGGGCGGGTCCAGGCTATGGATGGGAGA	105	226	TTCAAAGCAGTCACTCAGACAAACCAAGGGTGTCTCTGTGGCCACAAACCAACCAAGAGTCGA	285
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Db GTCAGATTCCAA 1677

RESULT 7
US-09-978-608A-258
; Sequence 258, Application US/0978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James,
; APPLICANT: Paoloni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 258
; LENGTH: 2764
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-608A-258

Query Match 70.2%; Score 1078.8; DB 10; Length 2764;
Best Local Similarity 81.4%; Pred. No. 0;
Matches 1329; Conservative 0; Mismatches 207; Indels 96; Gaps 3;

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavitt, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C4
CURRENT APPLICATION NUMBER: US/09/978,191A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
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PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
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PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
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PRIOR FILING DATE: 1998-03-30
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PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366

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DB 1666 GTCAAGTTCCAA 1677

RESULT 10

US-09-978-403A-258
Sequence 258, Application US/09978403A
Publication No. US20030050240A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C17
CURRENT APPLICATION NUMBER: US/09/978,403A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797

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RESIST 11

RESULT II
IC-09-978-564A-259

JS-09-978-564A-258
Sequence 258, Application US/09978564A

Sequence 258, Application US/09110000, Publication No. US20030050241A1

PUBLICATION NO. USZU
GENERAL INFORMATION:

GENERAL INFORMATION:
APPLICANT: Ashkenazi Avi

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker, Kevin p.

APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David

APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc

APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan

APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napol

APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen

APPLICANT: Filvaroff, Ellen
APPLICANT: Fong Sherman

APPLICANT: Fong, Sherman
APPLICANT: Gao Wei-Qiang

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Andrew

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.

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 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

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;	PRIOR APPLICATION NUMBER: 60/084643	
;	PRIOR FILING DATE: 1998-05-07	
;	PRIOR APPLICATION NUMBER: 60/085339	
;	PRIOR FILING DATE: 1998-05-13	
;	PRIOR APPLICATION NUMBER: 60/085338	
;	PRIOR FILING DATE: 1998-05-13	
;	PRIOR APPLICATION NUMBER: 60/085323	
;	PRIOR FILING DATE: 1998-05-13	
;	PRIOR APPLICATION NUMBER: 60/085582	
;	PRIOR FILING DATE: 1998-05-15	
;	PRIOR APPLICATION NUMBER: 60/085700	
;	PRIOR FILING DATE: 1998-05-15	
;	PRIOR APPLICATION NUMBER: 60/085689	
;	PRIOR FILING DATE: 1998-05-15	
;	PRIOR APPLICATION NUMBER: 60/085579	
;	PRIOR FILING DATE: 1998-05-15	
;	PRIOR APPLICATION NUMBER: 60/085580	
;	PRIOR FILING DATE: 1998-05-15	
;	PRIOR APPLICATION NUMBER: 60/085573	
;	PRIOR FILING DATE: 1998-05-15	
;	PRIOR APPLICATION NUMBER: 60/085704	
;	PRIOR FILING DATE: 1998-05-15	
;	PRIOR APPLICATION NUMBER: 60/085697	
Query Match 70.2%; Score 1078.8; DB 10; Length 2764;		
Best Local Similarity 81.4%; Pred. No. 0;		
Matches 1329; Conservative 0; Mismatches 207; Indels 95; Gaps 3		
QY	1	ATGCTACTGCCACATGCTGCTGTCCTCGCTGCTGGCGGGTCCAGGCTATGATGGGAGA 60
Db	46	ATGCTACTGCCACATGCTGCTGTCCTCGCTGCTGGCGGGTCCAGGCTATGATGGGAGA 105
QY	61	TTCTGGATAACAGTGCAGGAGTCAGTGATCGTCCGGAGGGGCTGTGCACTCTCTGTGCC 120
Db	106	TTCTGGATAACAGTGCAGGAGTCAGTGATGCTCCGGAGGGGCTGTGCACTCTCTGTGCC 165
QY	121	TGCTCTTTCTCCTACCCCGACAGGACTGGACAGGGTCTACCCAGCTTATGGCTACTGG 180
Db	166	TGCTCTTTCTCCTACCCCGACAGGACTGGACAGGGTCTACCCAGCTTATGGCTACTGG 225
QY	181	TTCAAAGCAGTGACTGAGACAAACCAAGGGTGCTCTGTGGCCACAAACCAACAGAGTCGA 240
Db	226	TTCAAAGCAGTGACTGAGACAAACCAAGGGTGCTCTGTGGCCACAAACCAACAGAGTCGA 285
QY	241	GAGGTGGAAATGAGCACCCCGGGCCGATTCCAGCTCACTGGGATCCCGCCAAAGGGGAAC 300
Db	286	GAGGTGGAAATGAGCACCCCGGGCCGATTCCAGCTCACTGGGATCCCGCCAAAGGGGAAC 345
QY	301	TGCTCTTTGGTGATCAGAGACGGCAGATGCAGATGAGTCAAGTACTTCTTTGGGGTG 360
Db	346	TGCTCTTTGGTGATCAGAGACGGCAGATGCAGATGAGTCAAGTACTTCTTTGGGGTG 405
QY	361	GAGAGAGAACTATGTGAGATATAATTCATGAACGATGGGTCTCTTCTAAAAAGTAACA 420
Db	406	GAGAGAGAACTATGTGAGATATAATTCATGAACGATGGGTCTCTTCTAAAAAGTAACA 465
QY	421	GCCCTGACTCAGAAGCCTGATGTCTACATCCCGAGACC----- 459
Db	466	GTGCTCAGCTTTCAGGCCCAAGACCCAGGACCAACACCGACCTCACCTGSCCATGTGGAC 525
QY	460	-----CTGGAGCCCGGSCACCGCTGACGGT 485
Db	526	TTTCTCCAAAGGGTGTGAGGACAGAGGACCGTCCGACTCGGTGGGCTATGCCCC 585
QY	486	CATCTGTGTGTTAACTGGGCTTTTGAGGAATGTCACCCCTTCTTTCTCTGAGCGGG 545
Db	586	AGAGACCTTGTTATCAGCATTTACGTTGACAAACAGCCAGGCTGGAGCCCGAGCCCCAG 645
QY	546	GGCTGCCCTCTCCTCCCAAGAACCAACCAAGACCTCCACTTCTCAGTGCTCAGCTT 605
Db	646	GGAATGTCCCATACCTGGAGGCCCAAAAGGCCAGTTCCTGGGGTCTCTCTGTGCTGCT 705
QY	606	CACGCCCAAGACCCAGGACCAC-----GACACGAGCCTCAC 641

706 GACAGCCAGCCCTCGCAGACTGAGTGGTCTGAGAAACAGAGTCTCTCTCGTCC 765
642 CTGCAATGTGACTTCTCCAGAAAGGTGTGAGGCAACAGAGACCGTCCGATCCGTTGT 701
766 CATCCCTGGGGCCCTAGACCCCTGGGCTGGAGTGCCTGGGTGAAGGTGGGATCA 825
702 GGCCTATGCCCCAGAGACCTTGTATCAGATTTCAGTGAACACAGCC----- 752
826 GGGCGCTACCTCCGAGCGGAGAACAGGCTGGCTCCAGAGAGAGCCCTGGACCTC 885
753 -----AGATCTCCAGAGAACTCAGAGTATGTTTCCCAAGCAACAGAGAGTC 804
886 TCTGTGAGTATCTCCAGAGAACTCAGAGTATGTTTCCCAAGCAACAGAGAGTC 945
805 CTGAAACCTTGGAAACGCGACGTCTCTCCAGTACTGAGGGCCAAAGCCTGTGCTG 864
946 CTGAAACCTTGGAAACGCGACGTCTCTCCAGTACTGAGGGCCAAAGCCTGTGCTG 1005
865 GTCTGTCTCACACAGAGACGCCCCCAGCCAGGCTGAGTGGACCCAGAGGGGACAGTT 924
1006 GTCTGTCTCACACAGAGACGCCCCCAGCCAGGCTGAGTGGACCCAGAGGGGACAGTT 1065
925 CTGAGCCCTTCCAGAGCTCAGAGCCCGGGTCTGAGTGGCTGCTGGTTCAGTGGAG 984
1066 CTGAGCCCTTCCAGAGCTCAGAGCCCGGGTCTGAGTGGCTGCTGGTTCAGTGGAG 1125
985 CACAGAGAGAGTTCAGTCCAGCTCGGACCCAGCTGGGCTCCAGAGAGTCTCTCTC 1044
1126 CACAGAGAGAGTTCAGTCCAGCTCGGACCCAGCTGGGCTCCAGAGAGTCTCTCTC 1185
1045 AGCTCTCTCGTGCATATAAGAGGAGTCACTCAACAGGATTCCTCAATGAGGCTT 1104
1186 AGCTCTCTCGTGCATATAAGAGGAGTCACTCAACAGGATTCCTCAATGAGGCTT 1245
1105 CTGGATCGGATCAGGCT 1164
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1465 GGCTCAGAGAGAGAGAGTATGATGTTCCGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1524
1606 GGCTCAGAGAGAGAGAGTATGATGTTCCGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1665
1525 GTCAAGTTCCAA 1536
1666 GTCAAGTTCCAA 1677

RESULT 12

US-09-999-833A-258

Sequence 258, Application US/09999833A

Publication No. US20030054405A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PLC65
CURRENT APPLICATION NUMBER: US/09/999,833A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
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PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
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PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728

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3	PRIOR APPLICATION NUMBER: 60/083558
4	PRIOR FILING DATE: 1998-04-29
5	PRIOR APPLICATION NUMBER: 60/083559
6	PRIOR FILING DATE: 1998-04-29
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9	PRIOR APPLICATION NUMBER: 60/083742
10	PRIOR FILING DATE: 1998-04-30
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15	PRIOR APPLICATION NUMBER: 60/084441
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22	PRIOR FILING DATE: 1998-05-07
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37	PRIOR APPLICATION NUMBER: 60/085382
38	PRIOR FILING DATE: 1998-05-15
39	PRIOR APPLICATION NUMBER: 60/085700
40	PRIOR FILING DATE: 1998-05-15
41	PRIOR APPLICATION NUMBER: 60/085689
42	PRIOR FILING DATE: 1998-05-15
43	PRIOR APPLICATION NUMBER: 60/085579
44	PRIOR FILING DATE: 1998-05-15
45	PRIOR APPLICATION NUMBER: 60/085560
46	PRIOR FILING DATE: 1998-05-15
47	PRIOR APPLICATION NUMBER: 60/085573
48	PRIOR FILING DATE: 1998-05-15
49	PRIOR APPLICATION NUMBER: 60/085704
50	PRIOR FILING DATE: 1998-05-15
51	PRIOR APPLICATION NUMBER: 60/085697

Query Match	70.2%	Score 1078.0;	Length 1367;
Best Local Similarity	81.4%;	Pred. No. 0;	
Matches 1329;	Conservative	0;	Mismatches 207; Indels 96; Gaps 3;

QY	1	ATGCTACTGCCACTGCTGCTGTCTCTCTGCTCTGGGGGGTCCAGAGCTATGGATGGAGA	60
Db	46	ATGCTACTGCCACTGCTGCTCTCTCTGCTGCGGGGGTCCAGAGCTATGGATGGAGA	105
QY	61	TTCTGGATACAGTGCAGGAGTCAAGTATGGTCCCGAGAGGCGCTGTGCATCTCTGTGCCC	120
Db	106	TTCTGGATACAGTGCAGGAGTCAAGTATGGTCCCGAGAGGCGCTGTGCATCTCTGTGCCC	165
QY	121	TGCTCTTTTCTCTTACCCCGCAGAGACTGGACAGGGTCTACCCACAGTTATGGCTACTGG	180
Db	166	TGCTCTTTTCTCTTACCCCGCAGAGACTGGACAGGGTCTACCCACAGTTATGGCTACTGG	225
QY	181	TTCAAAGCAGTGTACTGAGACAAACCAAGGGTGCTCTGTGCGCCACAAACACACAGATCGA	240
Db	226	TTCAAAGCAGTGTACTGAGACAAACCAAGGGTGCTCTGTGCGCCACAAACACACAGATCGA	285
QY	241	GAGGTGGAAATGAGCACCCCGGGGCGGATTCCAGTCACTGGGGATCCCGCCAAAGGGGAAC	300

DB 286 GAGGTGGAATGAGCACCGGGCGGATCCAGCTCACTGGGATCCCGCAAGGGGAC 345
QY 301 TGCTCTCTGGTGATCAGAGACCGCAGATGAGGATGAGTACAGTACTTCTTTCGGGTG 360
DB 346 TGCTCTCTGGTGATCAGAGACCGCAGATGAGGATGAGTACTTCTTTCGGGTG 405
QY 361 CAGAGAGAACTAGTGAATATAATTTATGAACTAGTGGTCTTCTTAAAGTAACA 420
DB 406 CAGAGAGAACTAGTGAATATAATTTATGAACTAGTGGTCTTCTTAAAGTAACA 465
QY 421 GCCCTGACTCAGAGCTGTGTACATCCCGAGAC----- 459
DB 466 GTGCTCAGCTTACGCCCCAGACCCAGGACCAACACCGACCTCCTGCCATGTGGAC 525
QY 460 -----CTGAGCCCGGGCAGCCGGTGACGGT 485
DB 526 TTCTCCAGAAAGGCTGTAGCGCACAGAGACCGTCCGACTCCGCTGTGGCTATGCCCC 585
QY 486 CATCTGTGTGTTAACTGGGCTTTGAGGATGTCCACCCCTTCTTCTCTGAGCGG 545
DB 586 AGAGACCTTGTATCAGCATTTACGTTGACAAACACGCGCCCTGGAGCCCCAGCCCCAG 645
QY 546 GGCTGCCCTCTCTCCCAAGAAACCAACCAACCTCCCACTTCTCAGTGTCTCAGCTT 605
DB 646 GGAAATGTCCCATACCTGGAAGCCCAAAAGGCCAGTTCCTGGCGCTCCTCTGTGCTGT 705
QY 606 CACGCCCAGACCCAGACAC-----GACACCGACCTCAC 641
DB 706 GACAGCCAGACCCCTGACACTGAGTGGGTCTCTGAGAACAGAGTCTCTCTCTGCTCC 765
QY 642 CTGCGCATGTGCACTTCTCCAGAAAGGCTGTGAGGACACAGAGACCGTCCGACTCCGCTGT 701
DB 766 CATCTCTGGGCTTAGACCCCTGGGCTGAGGCTGCGCGGGTGAAGGTGGGATTC 825
QY 702 GGCCTATGCCCGCCAGAGACCTTGTATCAGATTTACGTGACAAACAGCC----- 752
DB 826 GGGCGCTACACCTCCGAGCGGAGAAACAGGCTTGGCTCCAGAGAGAGCCCTGAGCCTC 885
QY 753 -----AGATCTCCAGAGACCTCAGAGTGTGTTTCCAGCAACAGAGCAGTC 804
DB 886 TCTGTGAGTATCTCCAGAGACCTCAGAGTGTGTTTCCAGCAACAGAGCAGTC 945
QY 805 CTGGAACCTTGGGAACCGCACCTCTCTCCAGTACTGAGGCGCCAAAGCCTGTGCTG 864
DB 946 CTGGAACCTTGGGAACCGCACCTCTCTCCAGTACTGAGGCGCCAAAGCCTGTGCTG 1005
QY 865 GTCTGTGTACACAGAGCCCCCAGCAGGCTGAGTGGACCCAGAGGGGACAGGTT 924
DB 1006 GTCTGTGTACACAGAGCCCCCAGCAGGCTGAGTGGACCCAGAGGGGACAGGTT 1065
QY 925 CTGAGCCCTTCCAGCCCTCAGACCCCGGGTCTCTGAGTGTGCTCGGTTCAAGTGGAG 984
DB 1066 CTGAGCCCTTCCAGCCCTCAGACCCCGGGTCTCTGAGTGTGCTCGGTTCAAGTGGAG 1125
QY 985 CACGAAGAGGTTACCTGCGAGCTGCGACCCAGCAGGCTGAGTGGACCCAGAGGGGACAGGTT 1044
DB 1126 CACGAAGAGGTTACCTGCGAGCTGCGACCCAGCAGGCTGAGTGGACCCAGAGGGGACAGGTT 1185
QY 1045 AGCTCTCCGTGACTAAGAGGGGACTCATCTCAAGGCACTTCTCCAATGAGGCTTT 1104
DB 1186 AGCTCTCCGTGACTAAGAGGGGACTCATCTCAAGGCACTTCTCCAATGAGGCTTT 1245
QY 1105 CTGGAAATGCGCATCAGGCTCTCTTTTCTCTGCTGCGCTGATCATCATGAAGATT 1164
DB 1246 CTGGAAATGCGCATCAGGCTCTCTTTTCTCTGCTGCGCTGATCATCATGAAGATT 1305
QY 1165 CTACCGAGAGAGGCTCAGACAGAAACCCCGAGGCCAGGTTCTCCGCGACAGCAGC 1224
DB 1306 CTACCGAGAGAGGCTCAGACAGAAACCCCGAGGCCAGGTTCTCCGCGACAGCAGC 1365
QY 1225 ATCTGGAATATCATCAATGTGGTCCCGAGCGCTGCGCCCTTGCTCAGAGCGGAATCAG 1284

DB 1366 ATCTGGAATATCATCAATGTGGTCCCGAGCGGTGCCCCCTGCTCAGAGCGGAATCAG 1425
QY 1285 AAAGCCACACCAAAACAGTCTCTCGGACCCCTCTTCCACAGGTTGCTCTCCCGCAGAAATCA 1344
DB 1426 AAAGCCACACCAAAACAGTCTCTCGGACCCCTCTTCCACAGGTTGCTCTCCCGCAGAAATCA 1485
QY 1345 AAGAAGAACCCAGAAAAGCAGTATCAGTTGCCAGTTTCCAGAACCCAAATCATCTACT 1404
DB 1486 AAGAAGAACCCAGAAAAGCAGTATCAGTTGCCAGTTTCCAGAACCCAAATCATCTACT 1545
QY 1405 CAAGCCCCAGAAATCCAGAGAGGCAAGAGAGCTTCAATATGCCACGCTCAACTTCCCA 1464
DB 1546 CAAGCCCCAGAAATCCAGAGAGGCAAGAGAGGCTTCAATATGCCACGCTCAACTTCCCA 1605
QY 1465 GCGCTCAGACCCAGCCCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATATGCGAGAA 1524
DB 1606 GCGCTCAGACCCAGCCCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATATGCGAGAA 1665
QY 1525 GTCAGGTTCCAA 1536
DB 1666 GTCAAGTTCCAA 1677

RESULT 13

US-09-981-915A-258
; Sequence 258, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C12
; CURRENT APPLICATION NUMBER: US/09/981.915A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
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APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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; Publication No. US20030060406A1
; GENERAL INFORMATION:
; APPLICANT: Askenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mackey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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8: gb_gssi:*
9: gb_gssi2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	478	31.1	667	6	CB534607 WMSPO040
4	448.8	29.2	514	5	EX470328 DKFZ5779N
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6	372.8	24.3	1745	4	BM906520 AGENCOURT
7	338	22.0	2017	3	AK042488 Mus muscu
8	324.8	21.1	1313	3	CR614233 full-length
9	324.8	21.1	1821	3	CR600025 full-length
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12	307.2	20.0	505	5	EX283650 BX283650
13	307.2	20.0	936	2	BF663289 602144414
14	301.6	19.6	3939	3	AK036698 Mus muscu
15	296.8	19.3	1121	4	BM564074 AGENCOURT
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24	276	18.0	1012	4	BM922958 AGENCOURT

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ALIGNMENTS

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clone CS0DI025YC24 5-PRIME, mRNA sequence.
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VERSION BX345667 GI:46290734
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (Bases 1 to 1011)
AUTHORS Li.W.B., Gruber.C., Jesse.J. and Polayes.D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 5, 2003 this sequence version replaced gi:30373021.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of invitrogen. This sequence belongs to sequence cluster
9384.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0A1025BB12QPl&c=9384.r.

FEATURES

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/db_xref="taxon:9606"
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/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 36.8%; Score 565.4; DB 5; Length 1011;
Best Local Similarity 77.7%; Pred. No. 2.1e-141;
Matches 750; Conservative 4; Mismatches 160; Indels 51; Gaps 4;


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QY 422 CCTGACTCAGAAAGCCTGATGCTACATCCCGAGACCCCTGGAGCCGCGCAGCCGGTGA 481
Db 466 CCTGACTCAGAAAGCCTGATGCTACATCCCGAGACCCCTGGAGCCGCGCAGCCGGTGA 525
QY 482 CGGTCACTGTGTGTTAACTGGGCTTTGAGAAATGTCCACCCCTTCTTCTCTCTGGA 541
Db 526 CGGTCACTGTGTGTTAACTGGGCTTTCAAGAAATGTCCAGCCCTTCTTCTCTCTGGA 585
QY 542 CGGGGGTGCCTCTCTCCCTCAAGGAACCAACCAAGACCTCCCACTTCTCAGTCTCA 601
Db 586 CGGGGGTGCCTCTCTCCCTAGAGAACAGACCAAGACCTCCCACTTCTCAGTCTCA 645
QY 602 GTTTCAGCCAGACCCAGGACCAAGACCAAGACCTCACTCCATGTGGACTTCTCCA 661
Db 646 GTTTCAGCCAGACCCAGGACCAAGACCAAGACCTCACTCCATGTGGACTTCTCCA 705
QY 662 GAAAGGTGTGAGCGACAGACAGCGT-CCGACTCCGTGGCCT 706
Db 706 GAAAGGTGTGAGCGACAGACAGCGTCCCGACTCCGTGGCCT 751

RESULT 3
CB554607
LOCUS
DEFINITION
WMSPO040_D05 WMSP Macaca mulatta cDNA, mRNA sequence.
ACCESSION
CB554607.1 GI:31303802
VERSION
EST.
KEYWORDS
SOURCE
Macaca mulatta (rhesus monkey)
ORGANISM
Macaca mulatta
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
REFERENCE
1 (bases 1 to 667)
Katz, M.G., Bungartner, R., Korth, M., Feldman, R., Amjadi, M. and
Holzman, T.
Expressed sequence tags from Rhesus macaque spleen
Unpublished (2002)
Contact: Holzman T
Katz Lab
University of Washington
Box 358070, Seattle, WA 98195-8070, USA
Tel: 206 732 6156
Fax: 206 732 6055
Email: ted@locke.hs.washington.edu
Similar to GenBank entry AF311905 AF311905 Homo sapiens sialic
acid-binding Ig-like lectin 10 (SIGLEC10) mRNA, complete cds.
8/2001
Plate: WMSPO040 row: D column: 05.
FEATURES
source
1..667
/organism="Macaca mulatta"
/mol_type="mRNA"
/db_xref="taxon:9544"
/sex="male"
/cell_type="monocytes"
/dev_stage="adult"
/clone_lib="WMSP"
/notes="Organ: spleen"

Query Match 31.1%; Score 478; DB 6; Length 667;
Best Local Similarity 94.8%; Pred. No. 8.3e-118;
Matches 506; Conservative 0; Mismatches 25; Indels 3; Gaps 1;

QY 1006 CAGCTCGGACCCACTGGGCTCCAGCAGCTCTCTCAGCCTCTCCGTGCACATAAG 1065
Db 1 CAGCTCAGACCCCGTGGTGGTCTCAGCAGCTCTCTCAGCCTCTCCGTGCACATAAG 60
QY 1066 AAGGACTCATCTCAACCGCATCTCCAAATGGAGCGTTTCTGGGAATCGGCATCAGCGCT 1125
Db 61 AAGGACTCATCTCAACCGCATCTCTCCAGCGAGCGTTTCTGGGAATCGGCATCAGCGCT 120
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```
QY 1126 CTTCTTTTCTCTGCTGGCCCTGATCATCATGAAGATTCTACCGAAGAGACGACTCAG 1185
Db 121 CTTCTTTTCTCTGCTGGCCCTGATCATCATGAAGATTCTACCAAGAGACGACTCAG 180
QY 1186 ACAGAAACCCGAGCCCGAGTTCTCCGGCAGCAGCATCTCGGATTAATCATCATGTG 1245
Db 181 GCAGATACCCCAAGGCCCGAGTTCTCCGGCAGCAGCATCTCGGATTAATCATCATGTG 240
QY 1246 GTCCCGAGCGGTGGCCCTGGCTCAGAAAGCGGAATCAGAAAGCCACACCAAGAGTCT- 1303
Db 241 GTCCCGAAGGCGGGCCCTGGCTCAGAAATCAGAAAGCCACACCAAGAGTCTCT 300
QY 1304 -CTCGAGCCCTCTTTCACAGGTGCTCCCTCCCGAGAAATCAAAAGAAACAGAAAAAG 1362
Db 301 TCTCGAGCCCTCTTTCACAGGTGCTCCCTCCCGAGAAATCAAAAGAAACAGAAAAAG 360
QY 1363 CAGTATCAGTTGCGCAGTTTCCAGAACCCAAATCATCTCAAGCCCGCAGATCCCGAG 1422
Db 361 CAGATCAGTTGCGCAGTTTCCAGAACCCAAATCATCTCAAGCCCGCAGATCCCGAG 420
QY 1423 GAGAGCCCAAGAGGAGCTCCATTATGCCACGCTCACTTCCAGGCGTCAGACCCAGGCT 1482
Db 421 GAGAGCCCAAGAGGAGCTCCATTATGCCACGCTCACTTCCAGGCGTCAGACCCAGGCT 480
QY 1483 GAGGCCCGGATGCCCAAGGCGACCCAGGCGGATTCGAGAGCACTCAAGTTCCAA 1536
Db 481 GAGGCTGGATGCCCAAGGCGACCCAGGCGGATTCGAGAGCACTCAAGTTCCAA 534

RESULT 4
CB470328
LOCUS
DEFINITION
DKFZp779N169_r1 779 (synonym: hnccl) Homo sapiens cDNA clone
ACCESSION
CB470328
VERSION
BX470328.1 GI:32023094
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 514)
Bloecker, H., Boecker, M., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
Fobo, G., Han, M. and Wiemann, S.
EST (Bloecker, H., Boecker, M., Mewes, H.W., Weil, B., Amid, C., et al.)
Unpublished (2003)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No s1 sequence available.
This clone (DKFZp779N169) is available at the RZPD in Berlin.
Please contact the RZPD, Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
source
1..514
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp779N169"
/tissue_type="liver"
/dev_stage="fetal"
/lab_host="DH10B"
/clone_lib="779 (synonym: hnccl)"
/notes="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIB"

ORIGIN
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FEATURES
high quality sequence stop: 421.
Location/Qualifiers
1..1464
/organism="Homo sapiens"
/label_type="taxon"
/cb="X"
/cb_xref="taxon"
/clone="IMAGE:5587773"
/lab_host="OH103"
/clone_lib="NH MGC 125"

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BM906520	EM906520.1	GI:19356899
ACCESSION	VERSION	EST.
KEYWORDS	SOURCE	ORGANISM
	Homō sapiens (human)	
	Homō sapiens	
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
REFERENCE	1 (bases 1 to 1745)	

AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>,
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabbs@mail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM12364 row: o column: 15
High quality sequence start: 64
High quality sequence stop: 538.
Location/Qualifiers
1..1745
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5590502"
/lab_host="DHIOB"
/clone_lib="NIH_MGC_125"
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."

FEATURES
source
Query Match 24.3%; Score 372.8; DB 4; Length 1745;
Best Local Similarity 82.3%; Pred. No. 3.2e-99;
Matches 428; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

ORIGIN

QY 2 TGCTACTGCACTGTGTCCTCGCTGCTGGCGGGTGCCAGGCTATGGATGGAGAT 61
DB 107 TGTCTGTCGCCCTGCTGCTGCCGCTGCTGGCGGGTGCTCCTGAACAGATCCCAGTT 166
QY 62 TTGTGATAGCTGAGAGAGTCAGTAGTGTGTCGGAGGGCTGTGATCTCTGTGCCCT 121
DB 167 ACAGTCTTCAAGTCAGAGCGCAGGTGTCGGGTGTCGGAGGGCTGTGTGTCATGTCCTT 226
QY 122 GTCTTTTCTCCACCACCCGACAGGACTGGACAGGTCTACCCAGCTATTGGCTACTGGT 181
DB 227 GAACCTCTCTACCCCGGGATGCTGGACGAGTCTACTGCTGCTTATGGCTACTGGT 286
QY 182 TCAAAGACGTGACTGAGAACCAAGGTGCTCTGTGGCCACAACCAACAGAGTCGAG 241
DB 287 TCAAAGACGGACCGCCAAAGACGGTGCTCTGTGGCCACTAACAACAGAGTCGAG 346
QY 242 AGGTGGAATGACACCGGGCGCATTCACGCTCACTGGGATCCCGCAAGGGAGCT 301
DB 347 AGGTGCAATGACACCGGGACCATTCACGCTCACTGGGATCCCGCAAGGGAGCT 406
QY 302 GTCTCTTGTGATCAGACGCGCAGATCGAGGATGAGTCACAGTACTTCTTCGGGTGG 361
DB 407 GCTCTTGTGATCAGACGCGCAGAGGAGGATGAGCATGTGCTTCTTCGGGTGG 466
QY 362 AGAGGAGAGCTATGTGAGATAATATTCATGACGATGGTCTTCTTAAGTAAACAG 421
DB 467 AGAGAGGAGAGCGCTGTGAGACATAGTCTTCCTGACGATGCGTCTTCTTAAGTAAACAG 526
QY 422 CCTGACTCAGAAGCTGATGCTACATCCCGGACACCGCTGGCGGGCAGCGCGGTGA 481
DB 527 CCTGACTCAGAGGCTGATGCTACATCCCGGACACCGCTGGCGGGTTCAGCGGTGA 586
QY 482 CGGTCACTGTGTGTTTAACTGGGCTTTGAGGAATGCC 521
DB 587 CGTTCATCTGTGGTTTAACTGGGCTTTTAAAGATGTC 626

Db	862	---CCAAGGAACAGCGCAGCCTTCAAAATCTGTGAAAACACCTGTCCTCCTGTCCT	918
Qy	843	GGAGGGCCAAAGCCTGTGCTGTGTGTGTGTACACACAGCAGCCCCCCCCACCCAGGTGAG	902
Db	919	GGAGGGCCAGGCTCTCGGCTGTCTGTGTATGTGACGGCAACCCCTGCACACCTGAG	978
Qy	903	CTTGACCCAGAGGGGACAGGTTCTGTAGACCCCTCCAGCCCTCAGACCCGGGTCCTGGA	962
Db	979	CTGGTTCCAGGGGTTCCCGCCCTGAACGCCACCCCATCTCCAATACCGGGGTCTGGA	1038
Qy	963	GTCGCTCGGGTTCAAAGTGGAGCAGCAAGAGAGTTCACTGCGACGCTCGGCACCCACT	1022
Db	1039	GCTGCTCAAGTAGGCTCTGCAGAAAGAGATTTCACCTGCGTCTCAGCATCCTCT	1098
Qy	1023	GGGCTCCAGCAGCGTCTCTTAGCCTCTCCGTGCACTATAGAAGGACTCATCTCAAC	1082
Db	1099	GGGCTCCCTGCAATCTCTCAGTCTCTTTGTGCAATGGAAACCGAAGCGCAGGCTGG	1158
Qy	1083	GGCATCTCCAATGGAGCGTTTCTGGGAATCGGCATCAGCGCTTCTTTCTCTGTCCT	1142
Db	1159	TGTTGT---CCTGGGAGCAGTCTGGGAGCTAGCATCAACCCCTGGTTTCTCTGTGT	1215
Qy	1143	GGCCCTGATCATCA---TGAAGATTCTACGAAGACCGGACTCAGACAG	1189
Db	1216	TTGCTTCATCTTCAGAGTGAAGACTAGAAGAAAGAACGAGCCAGCCAG	1265

RESULT 9

CR600025

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

ORIGIN

CR600025

full-length cDNA clone CS0DE012YC06 of Placenta of Homo sapiens (human).

CR600025

CR600025.1

GI:50480832

HTC; CNSLT_CDNA.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1821)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Paraday Avenue

2 (bases 1 to 1821)

Genoscope.

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers

1..1821

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DE012YC06"

/tissue_type="placenta"

/plasmid="pCMVSPORT_6"

Query Match

Best Local Similarity

Matches

714; Conservative

21.1%; Score 324.8; DB 3; Length 1821;

60.8%; Pred.No. 3.1e-76;

0; Mismatches 392; Indels 84; Gaps 7;

3 GCTACTGCCACTGCTGCTCTCGTGTGTCGGCGGGTCCAGGCTATGATGGAGATT

62

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de

This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
PCMV-M13u. Primer sequence: CGTGTAAACGACGGCGCGT.

FEATURES

source
1..505
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4297851"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 20.0%; Score 307.2; DB 5; Length 505;
Best Local Similarity 99.0%; Pred. No. 1.3e-71;
Matches 309; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 750 GCCAGATCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAAACAGGACAGCTCTGGA 809
Db 6 GCAGTATCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAAACAGGACAGCTCTGGA 65
QY 810 AAACCTTGGGAAACGGACAGCTCTCTCCAGTACTGAGGGCCAAAGCTGTGCTGTCTG 869
Db 66 AAACCTTGGGAAACGGACAGCTCTCTCCAGTACTGAGGGCCAAAGCTGTGCTGTCTG 125
QY 870 TGTACACACAGACAGCCCGCCAGCGCTGAGCTGAGCCAGAGGGACAGGTTCTGAG 929
Db 126 TGTACACACAGACAGCCCGCCAGCGCTGAGCTGAGCCAGAGGGACAGGTTCTGAG 185
QY 930 CCCTCCCGACCTCAGACCCCGGGTCTGAGAGTGCCTCGGGTTCAAGTGGAGCAGCA 989
Db 186 CCCTCCCGACCTCAGACCCCGGGTCTGAGAGTGCCTCGGGTTCAAGTGGAGCAGCA 245
QY 990 AGGAGAGTTACCTGCGACCTCGGCACCCACTGGGCTCCAGCAGCTCTCTCAGCCT 1049
Db 246 AGGAGAGTTACCTGCGACCTCGGCACCCACTGGGCTCCAGCAGCTCTCTCAGCCT 305
QY 1050 CTCGGTGCACCTA 1061
Db 306 CTCGGTGCACCTA 317

RESULT 13

BF663289
LOCUS 60214414F1 NIH_MGC_48 936 bp mRNA linear EST 21-DEC-2000
DEFINITION mRNA sequence.
ACCESSION BF663289
VERSION BF663289.1 GI:11937171
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 936)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1152 row: k column: 04
High quality sequence stop: 661.

FEATURES

source
1..936
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4297851"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 20.0%; Score 307.2; DB 2; Length 936;
Best Local Similarity 99.0%; Pred. No. 1.5e-71;
Matches 309; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 750 GCCAGATCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAAACAGGACAGCTCTGGA 809
Db 13 GCAGTATCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAAACAGGACAGCTCTGGA 72
QY 810 AAACCTTGGGAAACGGACAGCTCTCTCCAGTACTGAGGGCCAAAGCTGTGCTGTCTG 869
Db 73 AAACCTTGGGAAACGGACAGCTCTCTCCAGTACTGAGGGCCAAAGCTGTGCTGTCTG 132
QY 870 TGTACACACAGACAGCCCGCCAGCGCTGAGCTGAGCCAGAGGGACAGGTTCTGAG 929
Db 133 TGTACACACAGACAGCCCGCCAGCGCTGAGCTGAGCCAGAGGGACAGGTTCTGAG 192
QY 930 CCCTCCCGACCTCAGACCCCGGGTCTGAGAGTGCCTCGGGTTCAAGTGGAGCAGCA 989
Db 193 CCCTCCCGACCTCAGACCCCGGGTCTGAGAGTGCCTCGGGTTCAAGTGGAGCAGCA 252
QY 990 AGGAGAGTTACCTGCGACCTCGGCACCCACTGGGCTCCAGCAGCTCTCTCAGCCT 1049
Db 253 AGGAGAGTTACCTGCGACCTCGGCACCCACTGGGCTCCAGCAGCTCTCTCAGCCT 312
QY 1050 CTCGGTGCACCTA 1061
Db 313 CTCGGTGCACCTA 324

RESULT 14

AK036698
LOCUS AK036698
DEFINITION Mus musculus adult male bone cDNA, RIKEN full-length enriched
library, clone:9830164H23 product:weakly similar to SIALIC
ACID-BINDING LECTIN [Homo sapiens], full insert sequence.
ACCESSION AK036698
VERSION AK036698.1 GI:26331615
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

664 AAGGTGTGAGCGACAGGACCGTCCGACTCCGTGTGGCCATG 709
 820 A-----TGACACAAAGAGCTGTCCGACTAAGAGTGGCCCTGTG 859

RESULT 15

BM564074

LOCUS

DEFINITION

AGENCY

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BM564074
 AGENCY: NIH_MGC
 VERSION: 1
 KEYWORDS: EST
 SOURCE: Homo sapiens (human)
 ORGANISM: Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1121)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
 DNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LUCM2014 row: e column: 11
 High quality sequence stop: 609.
 Location/Qualifiers
 1..1121
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5484658"
 /tissue_type="natural killer cells, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_106"
 /note="Organ: Blood; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
 ORIGIN

240 AGTGCAGAGGAGACCCAGGGCCGATTCACCTCCTCGGTGATCCCTCAAGGAAACAATG 299
 303 CTCCTTTGGTATCAGAGAGCGCGAGATGAGTACAGTACTTTCTTTCGGGTGGA 362
 300 CTCCTTGAGCATCAGAGAGCGCGAGGAGGACAAACGTTTCATCTCTTTTGGTGGC 359
 363 GAGAGGAGCTATGTGAGATATAATTTTCATGACCATGGTTCCTTCTAAAGTACAGC 422
 360 GAGAGGAG---AACAAATTTAGTTACAAATATTCCTCGGTCTCTGTGTATGTGACAGC 416
 423 CTTGACTCAGAAAGCCTGTCTACATCCCGGAGACCTCGAGCCCGGCGAGCCGCTGAC 482
 417 CTTGACCCACAGCGCCGACATCTCTATCCCGGAGTTCTTAAAGTCTGGCCATCCAGCAA 476
 483 GGTATCTGTGTGTTTAACTGGGCTTTGAGGAAATGTCCACCCCTTCTTTCTCTGGAC 542
 477 CTTGACCTGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 536
 543 GGGGGCTGCT 602
 537 GTCAGTCT 590
 603 CTTGACCCACAGCGCCGACAGGACCAACCAACCAACCAACCAACCAACCAACCAACCA 662
 591 GATCATCT 650
 663 AAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCGGTGGCCCTATGCCCCCAGAGACT 722
 651 AGCTGGTGTGACCGAGAGAAACATCCAGCTCAGTGTCTCTCTCTCTCTCTCTCTCTCT 710
 723 TGTATCAGCATTTTCAAGTGTGACCAACCAACCAACCAACCAACCAACCAACCAACCA 782
 711 AGTGATTCAAGCT 770
 783 TT 784
 771 TT 772

Search completed: November 8, 2004, 20:31:57
 Job time : 7201.25 secs

Query Match

Best Local Similarity 19.3%; Score 296.8; DB 4; Length 1121;

Matches 500; Conservative 0; Mismatches 272; Indels 10; Gaps 3;

3 GCTACTGCCACTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 62
 1 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 59
 63 CTGGATCAGAGTCCAGAGTCACTGATGTTGCGGAGGCTGCTGCTGCTGCTGCTGCTGCT 122
 60 CCGGCTGGAGATCCAGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCG 119
 123 CTCCTTCT 182
 120 TTCCGCTTCT 179
 183 CAAAGCAGTGTGATGAGACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 242
 180 CCGGAAAGGGTTCAGTGTAGACAGGAGACTCCAGTGGCCACCAACCAACCAACCAAC 239
 243 GGTGGAATGAGACCCCGGGCCGATTCAGTCTACTGGGATCCCGCAAGGGAATG 302

Result No.	Score	Query Match	Length	DB ID	Description
1	1917	100.0	3099	6	BD011516 Sialoadhe
2	1917	100.0	3099	6	BD011517 Sialoadhe
3	1907.4	99.5	2295	6	BD261703 12 human
4	1905.8	99.4	2126	9	AY032685 Homo sapi
5	1868	97.4	2954	6	AX036517 Sequence
6	1733	90.4	2208	6	AX365530 Sequence
7	1733	90.4	3012	9	AF301007 Homo sapi
8	1733	90.4	3024	6	AX365542 Sequence
9	1729.8	90.2	2176	6	AX365518 Sequence
10	1497.4	78.1	2823	6	AX365516 Sequence
11	1337	69.7	2565	6	CQ767791 Sequence
12	1333.8	69.6	2764	6	AX376050 Sequence
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471	GTGCTCAGCTTCAACGCCAGACCCAGGACCAACACCGGACCTCACTGCGCATGTGGAC	530
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1021	CTGAGCCCTCTCCAGCCCTCAGACCCCGGGGTCTCTGGAGCTGCTCTGGGTTCAGGTGGAG	1080
1071	CTGAGCCCTCTCCAGCCCTCAGACCCCGGGGTCTCTGGAGCTGCTCTGGGTTCAGGTGGAG	1130
1081	CACGAGAGAGATTCACTGTGCAACGCTGGGACCCCACTGGGCTCCCAAGCAAGTCTCTCTC	1140
1131	CACGAGAGAGATTCACTGTGCAACGCTGGGACCCCACTGGGCTCCCAAGCAAGTCTCTCTC	1190

QY	1141	AGCCTCTCCGTGCACTACTCCCGAAGCTGCTGGGGCCCTCTCTGCTCTCTCTGGGAGGCTGAG	1200
Db	1191	AGCCTCTCCGTGCACTACTCTCCCGAAGCTGCTGGGGCCCTCTCTGCTCTCTCTGGGAGGCTGAG	1250
QY	1201	GGTCTGCACTGCACTGCTCTCTCCAGGCGAGCCCGGCCCTCTCTGCGCTGCTGGTGGCTT	1260
Db	1251	GGTCTGCACTGCACTGCTCTCTCCAGGCGAGCCCGGCCCTCTCTGCGCTGCTGGTGGCTT	1310
QY	1261	GGGAGAGAGTGTGTGGAGGGGAAACAGCAGCCAGGACTCTTTGAGGTCAACCCCGAGCTCA	1320
Db	1311	GGGAGAGAGTGTGTGGAGGGGAAACAGCAGCCAGGACTCTTTGAGGTCAACCCCGAGCTCA	1370
QY	1321	GCAGGGCCCTGGGCGAACAGCTCCCTGAGCTCTCATGAGGGCTCAGCTCCGGCCCTCAGG	1380
Db	1371	GCAGGGCCCTGGGCGAACAGCTCCCTGAGCTCTCATGAGGGCTCAGCTCCGGCCCTCAGG	1430
QY	1381	CTCCGTGTGAGSCCTGGAACTGCTCACTGGGGCCAGAGTGGATCCATCTCTGAGCTGGCA	1440
Db	1431	CTCCGTGTGAGSCCTGGAACTGCTCACTGGGGCCAGAGTGGATCCATCTCTGAGCTGGCA	1490
QY	1441	GATAAGAGAGGACTCATCTCAACGGCATCTCCACCGGAGCGTTTCTGGGAATCGGCATC	1500
Db	1491	GATAAGAGAGGACTCATCTCAACGGCATCTCCACCGGAGCGTTTCTGGGAATCGGCATC	1550
QY	1501	ACGGCTCTCTTTTCTCTGCTTGGCTGGCCCTGATCATGAAGATTCTACCGAAGAGACGG	1560
Db	1551	ACGGCTCTCTTTTCTCTGCTTGGCTGGCCCTGATCATGAAGATTCTACCGAAGAGACGG	1610
QY	1561	ACTCAGACAGAAACCCGAGGCCAGGTTCTCCGGCAGCAGCAGATCTCTGATTTACATC	1620
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QY	1621	AATGTGTCTCCGACGGCTGGCCCTGGCTCGAAGCGGAATCAGAAAGCCACACCAAC	1680
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Db	1791	AACAGATATCAGTGTGCCAGTCTTCCAGAACCCAAATCATCCACTCAAGCCCCAGAACTC	1850
QY	1801	CAGGAGAGCAAGAGAGAGCTCCATATGCCAGCTCAACTCCCGAGGCTCAGACCCAGG	1860
Db	1851	CAGGAGAGCAAGAGAGAGCTCCATATGCCAGCTCAACTCCCGAGGCTCAGACCCAGG	1910
QY	1861	CTTGAGGCCCGGATGCCAAGGGCCACCGAGCGGATTATGCGAAGTCAAGTTCCAA	1917
Db	1911	CTTGAGGCCCGGATGCCAAGGGCCACCGAGCGGATTATGCGAAGTCAAGTTCCAA	1967
RESULT 2			
LOCUS	BD011517	3099 bp	DNA linear PAT 31-JAN-2002
DEFINITION	Sialoadhesin family 4 (SAF-4); cDNA.		
ACCESSION	BD011517		
VERSION	BD011517.1	GI:18639890	
KEYWORDS	JP 2001502359-A/2.		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
REFERENCE	1	(bases 1 to 3099)	
AUTHORS	Kikly, K.K. and Miller, C.L.E.		
TITLE	Sialoadhesin family 4 (SAF-4) cDNA		
JOURNAL	Patent: JP 2001502359-A 2 20-FEB-2001;		
COMMENT	SMITHKLINE BEECHAM CORP		
	OS Homo sapiens (human)		
	PN JP 2001502359-A/2		
	PD 20-FEB-2001		

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DB	1057	CTGGAAGACCTTGGGAAACCGGAGAACAGCTTTCCAGTACTTGGAGGGCCAAAGCCTTGGCTG	1116
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DB	1117	GTCTGTGTACACACAGACAGCCCGCCAGCCAGGCTGAGCTGACCCAGAGGGGACAGGTT	1176
QY	1021	CTGAGCCCTTCCAGAGCCCTCAGACCCCGGGGCTCTGGAGCTGCCTCGGGTTCAAGTGAG	1080
DB	1177	CTGAGCCCTTCCAGAGCCCTCAGACCCCGGGGCTCTGGAGCTGCCTCGGGTTCAAGTGAG	1236
QY	1081	CAGAGAGAGATTACCTGCCACGCTGGGACCCACTGGGCTCCACAGCTCTCTCTC	1140
DB	1237	CAGAGAGAGATTACCTGCCACGCTGGGACCCACTGGGCTCCACAGCTCTCTCTC	1296
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DB	1297	AGCCTCTCCGTGACACTCCCCGAAGCTGTGGGGCCCTCTCTGCTCTGGAGGCTGAG	1356
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DB	1477	GCCGGGCCCTGGGCCAAACAGCTCCTGAGCCTCCATGAGAGGCTCAGCTCCGGGCTCAGG	1536
QY	1381	CTCGGTGTGAGGCTTGGAGCTGCATGGGGCCAGAGTGGATCCATCTCAGGTGCCA	1440
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 QY 419 ----- 418
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 QY 419 ----- CAGTGTCT 426
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RESULT 7

AF301007 3012 bp mRNA linear PRI 26-JUL-2002
 AF301007 Homo sapiens sialic acid-binding immunoglobulin-like lectin 10
 LOCUS (SIGLEC10) mRNA, complete cds.

ACCESSION

AF301007

VERSION

AF301007.1

KEYWORDS

GI:21956185

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1. (bases 1 to 3012)

Whitney, G.S., Wang, S., Chang, H., Cheng, K.-Y., Liu, P., Zhou, X.D.,

Van, W.P. and Longphre, M.

A new Siglec family member, SIGLEC10, is expressed in cells of the

immune system and has signaling properties similar to CD33

Unpublished

2. (bases 1 to 3012)

Longphre, M., Whitney, G.S., Wang, S., Chang, H. and Van, W.P.

Direct Submission

Submitted (29-AUG-2000) Immunology Department, Bristol-Myers Squibb

Pharmaceutical Research Institute, Route 206 and Province Line

Road, Princeton, NJ 08543-4000, USA

FEATURES

Location/Qualifiers

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		ALDLVQYPPENLRVMSQANRTVLNGLTSLVLEQSLCLVQVCTHSSPPARLSW				Db			1078	TACACTGCGCAGCGAGAAACAGGCTT	1079	TGGCTCCAGCAGCAGGCTCTGGAATCTCTCTGTG
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APPLICANT: Gentz, Reiner L.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: CD33-Like Protein
FILE REFERENCE: 1488.0480001
CURRENT APPLICATION NUMBER: US/08/396.537A
CURRENT FILING DATE: 1997-07-18
PRIOR APPLICATION NUMBER: 60/022,481
PRIOR FILING DATE: 1996-07-19
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Sequence 5933, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 5933
LENGTH: 1473
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5933
Query Match 2.9%; Score 54.8; DB 4; Length 1473;
Best Local Similarity 50.0%; Pred. No. 0.00033;

	Matches	137;	Conservative	0;	Mismatches	137;	Indels	0;	Gaps	0;
Qy	1266	GGAGCTCTCGAGGGGAACACGACCCAGGACTCTCTCGAGTCA	CGCCCGGCTCAGCTCAGCGG	1325						
Db	640	GGTGACCTGTACGGCAACCATGATCTCTGAACTTCTGCGACTT	CGCCCGGCTCAGCTCAGCGG	581						
Qy	1326	GCCCTGGGGCAACAGCTCCCTGAGCTCCATGAGGGCTCAGTCC	CGGCTCAGGCTCCG	1385						
Db	580	CCGCGGCACCATCAGCTGCGCAACTTCTGGGGCTGCCGCTGAA	CTCTGCTGTTCCG	521						
Qy	1386	CTGTGAGGCTTGGAACTTCCATGGGGCCGACGAGTGGATCCAT	CTCGAGTGCACAGATAA	1445						
Db	520	CTCTTTCGCGTGCTCTCTCGCGCGGCCAGTTCAGGATCGACG	GCAGTCTCATCCAGAG	461						
Qy	1446	GAGGGACTCATCTCAACGCATCTCCACGGAGCGTTCTGGGAAT	CGGCATCAGCGC	1505						
Db	460	CCCCACCGACATCTGCGCGCGATGCCCGACACCCCTCTTCTGT	GCTGCTGCCAGCTGGC	401						
Qy	1506	TCTCTTTTCTCTGCTGGCCCTGTATCATCATG	1539							
Db	400	GCTGCTCATGTCACCGTGGCGGTGAACATCATG	167							

RESULT 11

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US-09-252-991A-5956
; Sequence 5956, Application US/0925299-A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5956
; LENGTH: 1809
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5956

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Query Match

Query Match	2.9%;	Score 54.8;	DB 4;	Length 1809;
Best Local Similarity	50.0%;	Fred. No. 0.00036;		
Matches 137;	Conservative 0;	Mismatches 137;	Indels 0;	Gaps 0;
QY	1266	GGAGCTGCTGGAGGGGAACAGCAGCAGGACTCCTTCGAGGTCAACCCCAAGCTCAGCCGG	1325	
Db	1041	GGTGACCTGTACGGGACCATTGCTGAACTTCTGCGACTTCGCCCGCGCTGCCCGGA	1100	
QY	1326	GCCTTGGGCCAAAGAGTCCCTGAGCCTCCATGAGGGCTCAGTTCGGCTCAGGCTCCG	1385	
Db	1101	CCGCGGACCATTACGGGTGCGCAACTTCTGGGGCTGCGGTGAACATCCTGCTGTTCGG	1160	
QY	1386	CTGTGAGGCGCTGGAAGCTCCATGGGCGCCAGAGTGTGATCCATCTCTGAGCTGCCAGATA	1445	
Db	1161	CTGTGTCGCGGTGGTCTCTCGCGCGGCCCGAGTTCAGGATCGACGGCCAGCTCATCCAG	1220	
QY	1446	GAAGGACATCATCTCAACGGCATTTCTCAACGAGAGGTTTCGGGAATCGGATCAGGC	1505	
Db	1221	CCCCACGACATCGTCGCGCGGATGCCCGACAACCTCTTCTCGTGTGCCAGCCTGGC	1280	
QY	1506	TCTCTTTTCTCTGCTGGCCCTGATCATCATG	1539	
Db	1281	GCTGTGTCATCGTCACCGTGGCGGTGAACATCATG	1314	

RESULT 12

US-09-252-991A-5939
; Sequence 5939, Application US/09252991A

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; Patent No. 6551795
;
; GENERAL INFORMATION:
;
; APPLICANT: Marc J. Rubenfield et al.
;
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;
; FILE REFERENCE: 107196.136
;
; CURRENT APPLICATION NUMBER: US/09/252,991A
;
; CURRENT FILING DATE: 1999-02-18
;
; PRIOR APPLICATION NUMBER: US 60/074,788
;
; PRIOR FILING DATE: 1998-02-18
;
; PRIOR APPLICATION NUMBER: US 60/094,190
;
; PRIOR FILING DATE: 1998-07-27
;
; NUMBER OF SEQ ID NOS: 33142
;
; SEQ ID NO 5939
;
; LENGTH: 2295
;
; TYPE: DNA
;
; ORGANISM: Pseudomonas aeruginosa
;
; US-09-252-991A-5939

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Query Match	2.9%;	Score 54.8;	DB 4;	Length 2295;
Best Local Similarity	50.0%;	Pred. No. 0.00039;		
Matches 137;	Conservative 0;	Mismatches 137;	Indels 0;	Gaps 0;
QY	1266	GGAGCTGCTGGAGGGAAACAGCAGCCAGGACTCCTTCGAGGTCACCCCGAGCTCAGCCGG	1325	
Db	1183	GGTGACCTGTACGGCACCATGATCTGAACTCTCGACTTCGCCCGGCTGCCCGGA	1242	
QY	1326	GCCTGGGGCAACAGTCCCTGAGCTCCATGAGAGGCTCAGTCCGGCCCTCAGGCTCCG	1385	
Db	1243	CCGCCCGCACCATCAGCGTCGGCAACTCTCGGGGGCTGCCGGTGAAATCATCTGCTGTTCGG	1302	
QY	1386	CTGTGAGGGCTCGAAACGTCCATCGGGGCCAGAGTGTGATCCATCCTCGAGCTGCCAGATAA	1445	
Db	1303	CCTGTTTCGGCGGTGGTCTCTCGCGCGGCCAGTTTCAGGATCGACGGCCAGCTCATCCAGAG	1362	
QY	1445	GAAGGAGCTCATCTCAAACGGCATTTCCAAACGAGAGGTTTCTGGGAATCGGATCAGGC	1505	
Db	1363	CCCCACGACATCGTCGCGCGGATCCCCGACACCCCTCTTCTCGTGTGCTGCCAGCTGGC	1422	
QY	1506	TCCTCTTTTTCCTCTGCCTGGCCCTGATCATCATG	1539	
Db	1423	GCTGCTGATCGTCACCGTGGCGGTGAACATCATG	1456	

RESULT 13

US-09-799-451-560
 ; Sequence 560, Application US/09799451
 ; Patent No. 6783969
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Zhou, Bing
 ; APPLICANT: Goodrich, Ryle
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Ren, Feiyang
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Xue, Aidong J.
 ; APPLICANT: Zhao, Qing A.
 ; APPLICANT: Wang, Jian-Rui
 ; APPLICANT: Ma, Yungqing
 ; APPLICANT: Yamazaki, Victoria
 ; APPLICANT: Chen, Rui-hong
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: Wang, Dunrui
 ; APPLICANT: Yang, Yonghong
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Ghoast, Reena
 ; APPLICANT: Drmanac, Radoje T.
 ; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
 ; FILE REFERENCE: 803
 ; CURRENT APPLICATION NUMBER: US/09/799,451
 ; CURRENT FILING DATE: 2001-03-05
 ; NUMBER OF SEQ ID NOS: 948

QY 1355 ATGGAGGGCTCAGCTCCGGCCTCAGGCTCCGCTGTGAGGC 1394
Db 437 CCTCCGGGCTACGCTACGACCCCGACATGGGGCGGAGGC 476

Search completed: November 8, 2004, 20:38:24
Job time : 208.523 secs

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61 TTCTGGATACGAGTGCAGGAGTCAGTGTGATGTCGCCGAGGCGCTGTGCATCTCTGTGCCC 120
118 TTCTGGATACGAGTGCAGGAGTCAGTGTGATGTCGCCGAGGCGCTGTGCATCTCTGTGCCC 177
121 TGCTCTTTCTCTACCCCGACAAAGACTGAGCAGGGTCTACCCAGCTTATGCTACTGG 180
178 TGCTCTTTCTCTACCCCGACAAAGACTGAGCAGGGTCTACCCAGCTTATGCTACTGG 237
181 TTCAAAGCAGTACTGAGACAACCAAGGGTCTCTGTGCCCCAACCAACACACAGAGTCGA 240
238 TTCAAAGCAGTACTGAGACAACCAAGGGTCTCTGTGCCCCAACCAACACACAGAGTCGA 297
241 GAGGTGAATAGACAACCCGGGGCCGATTCAGTCTCACTGGGATCCCGCCAAAGGGGAAC 300
298 GAGGTGAATAGACAACCCGGGGCCGATTCAGTCTCACTGGGATCCCGCCAAAGGGGAAC 357
301 TGCTCTTTGATGATCAGAGCGGCGAGATCAGAGTCAAGTACAGTACTTCTTCCGGTG 360
358 TGCTCTTTGATGATCAGAGCGGCGAGATCAGAGTCAAGTACAGTACTTCTTCCGGTG 417
361 GAGAGGAAGCTATGTAGATATAATTTTCATGAACGATGGTCTTCTTAAAGTAACA 420
418 GAGAGGAAGCTATGTAGATATAATTTTCATGAACGATGGTCTTCTTAAAGTAACA 477
421 GTGCTGAGCTTACGCCCCAGACCCAGGACCAACACACCGACCTCACTGCCATGTGGAC 480
478 GTGCTGAGCTTACGCCCCAGACCCAGGACCAACACACCGACCTCACTGCCATGTGGAC 537
481 TTCTCCAGAAAGGTTGTGAGCGCACAGAGACCGTCCGACTCCGCTGTGGCTATGCCCCC 540
538 TTCTCCAGAAAGGTTGTGAGCGCACAGAGACCGTCCGACTCCGCTGTGGCTATGCCCCC 597
541 AGAGACCTTGTATCAGCATTTCACTGACAAACACCGCAGCCCTGAGGCCACACGCCCAAG 600
598 AGAGACCTTGTATCAGCATTTCACTGACAAACACCGCAGCCCTGAGGCCACACGCCCAAG 657
601 GGAATCTCCATACCTGGAAGCCCAAAAGGCCAGTTCTCGGGCTCTCTGTGCTGTCT 660
658 GGAATCTCCATACCTGGAAGCCCAAAAGGCCAGTTCTCGGGCTCTCTGTGCTGTCT 717
661 GACAGCAGCCCTTGCACACTGTAGTGTGGTCTCTGAGAACAGATCTCTCTCTGCTCC 720
718 GACAGCAGCCCTTGCACACTGTAGTGTGGTCTCTGAGAACAGATCTCTCTCTGCTCC 777
721 CATCCCTGGGCGCTAGACCCCTGGGGCTGGAGCTCCCGGGTGAAGCTGGGATTCA 780
778 CATCCCTGGGCGCTAGACCCCTGGGGCTGGAGCTCCCGGGTGAAGCTGGGATTCA 837
781 GGGCGCTTACACCTGCCAGCGGAGACAGGCTTTGGCTCCCGAGCAGCGCCCTGGACCTC 840
838 GGGCGCTTACACCTGCCAGCGGAGACAGGCTTTGGCTCCCGAGCAGCGCCCTGGACCTC 897
841 TCTGTGAGTATCTCCAGAGACCTGAGAGTATGTTTCCCAACCAACAGGACAGTC 900
898 TCTGTGAGTATCTCCAGAGACCTGAGAGTATGTTTCCCAACCAACAGGACAGTC 957
901 CTGGAACCTTGGGAACGCGACGTCCTCCAGTACTGAGGGGCCAAAGCCCTGTGCTG 960
958 CTGGAACCTTGGGAACGCGACGTCCTCCAGTACTGAGGGGCCAAAGCCCTGTGCTG 1017
961 GTCTGTGTACACACAGACGCCCTCCAGCGAGCTGAGTGTGACCCAGAGGGGACAGGTT 1020
1018 GTCTGTGTACACACAGACGCCCTCCAGCGAGCTGAGTGTGACCCAGAGGGGACAGGTT 1077
1021 CTGAGCCCTTCCAGACCCCTCAGACCCCGGGTCTCTGAGTCTGCTCGGGTTCAAGTGGAG 1080
1078 CTGAGCCCTTCCAGACCCCTCAGACCCCGGGTCTCTGAGTCTGCTCGGGTTCAAGTGGAG 1137
1081 CAGAAAGGAGATTACCTGCCACGCTGGGACCCCACTGGGCTCCAGACGCTCTCTCTC 1140
1138 CAGAAAGGAGATTACCTGCCACGCTGGGACCCCACTGGGCTCCAGACGCTCTCTCTC 1197

1141 AGCTCTCTCGTGCATCTCTCCCGAAGCTGTGGGCCCCCTCTCTCTCTCTGGAGGCTGAG 1200
1198 AGCTCTCTCGTGCATCTCTCCCGAAGCTGTGGGCCCCCTCTCTCTCTCTGGAGGCTGAG 1257
1201 GGTCTGCACTCAGCTGCTCTCCAGGCCAGCCGGCCCCCTCTCTCTCTCTGGGCTGTGCTT 1260
1258 GGTCTGCACTCAGCTGCTCTCCAGGCCAGCCGGCCCCCTCTCTCTCTCTGGGCTGTGCTT 1317
1261 GGGGAGAGAGCTGCTGGAGGGGAACAGCAGCCAGGACTCTCTTCCAGAGTCAACCCCCAGCTCA 1320
1318 GGGGAGAGAGCTGCTGGAGGGGAACAGCAGCCAGGACTCTCTTCCAGAGTCAACCCCCAGCTCA 1377
1321 GCGGGCCCTTGGGCGCAACAGCTCTCTGAGCTCTCATGAGGGCTCAGCTCCGGGCTCAGG 1380
1378 GCGGGCCCTTGGGCGCAACAGCTCTCTGAGCTCTCATGAGGGCTCAGCTCCGGGCTCAGG 1437
1381 CTGCGCTGTGAGGCTTGAACGCTCATGGGGCCCGAGAGTGGATCCATCTCTGAGCTGCCA 1440
1438 CTGCGCTGTGAGGCTTGAACGCTCATGGGGCCCGAGAGTGGATCCATCTCTGAGCTGCCA 1497
1441 GATAAGAGAGAGCTCATCTCAACGGCATTTCTCAACGGAGGGTTCTGGGATCGGATC 1500
1498 GATAAGAGAGAGCTCATCTCAACGGCATTTCTCAACGGAGGGTTCTGGGATCGGATC 1557
1501 ACGCTCTCTTTCTCTCTGCTCTGCTGCTGATCATCATGAAGATTCTACCGAAGAGAGCG 1560
1558 ACGCTCTCTTTCTCTCTGCTCTGCTGCTGATCATCATGAAGATTCTACCGAAGAGAGCG 1617
1561 ACTCAGACAGAAACCCCGAGGCCAGGTTCTCCCGGCACAGCAGATCTCTGGATTATCATC 1620
1618 ACTCAGACAGAAACCCCGAGGCCAGGTTCTCCCGGCACAGCAGATCTCTGGATTATCATC 1677
1621 AATGTGCTCCGAGGCTGCGCCCTGCTCAGAGCGGATCAGAAAGCCACACCAAC 1680
1678 AATGTGCTCCGAGGCTGCGCCCTGCTCAGAGCGGATCAGAAAGCCACACCAAC 1737
1681 AGTCTCTCGAGCCCTCTTCCACAGAGTGTCTCCCTCCCGAGAAATCAAAAGAACACGAAA 1740
1738 AGTCTCTCGAGCCCTCTTCCACAGAGTGTCTCCCTCCCGAGAAATCAAAAGAACACGAAA 1797
1741 AAGCAGTATCAGTTGCCAGTTTCCGAGAACCCAAATCATCTCACTCAAGCCCGAGATCC 1800
1798 AAGCAGTATCAGTTGCCAGTTTCCGAGAACCCAAATCATCTCACTCAAGCCCGAGATCC 1857
1801 CAGGAGCCCAAGAGAGCTCCATTATGCCACGCTCAACTTCCAGGCGTCAGACCCAGG 1860
1858 CAGGAGCCCAAGAGAGCTCCATTATGCCACGCTCAACTTCCAGGCGTCAGACCCAGG 1917
1861 CCTGAGGCCCGATGCCCAAGGGCACCCAGCGGATTATGACAGAGTCAAGTTCCAA 1917
1918 CCTGAGGCCCGATGCCCAAGGGCACCCAGCGGATTATGACAGAGTCAAGTTCCAA 1974

RESULT 2

US-09-836-353A-15
; Sequence 15, Application US/09836353A
; Publication No. US20030129685A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF48921
; CURRENT APPLICATION NUMBER: US/09/836,353A
; PRIORITY FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 15
; LENGTH: 2295

907 AACCTTGGAAACGGACAGTCTCTCCAGTACTGGAGGGCCAAAGCCCTGTGCTGGTCTGT 966
1118 AACCTTGGAAACGGACAGTCTCTCCAGTACTGGAGGGCCAAAGCCCTGTGCTGGTCTGT 1177
967 GTCACACACAGCAGCCCGCCAGCAGCTGAGCTGGACCCAGAGGGGACAGGTTCTGAGC 1026
1178 GTCACACACAGCAGCCCGCCAGCAGCTGAGCTGGACCCAGAGGGGACAGGTTCTGAGC 1237
1027 CCCTCCAGCAGCTCAGACCCCGGGTCTCTGAGCTGCTCGGGTTCAAGTGGAGCAGAA 1086
1238 CCCTCCAGCAGCTCAGACCCCGGGTCTCTGAGCTGCTCGGGTTCAAGTGGAGCAGAA 1297
1087 GGAGAGTTACCTCCAGCTCGGACACCACTGGGCTCCAGCAGCTCTCTCTCAGCTC 1146
1298 GGAGAGTTACCTCCAGCTCGGACACCACTGGGCTCCAGCAGCTCTCTCTCAGCTC 1357
1147 TCCGTGCACTACTCCCGAAGCTCTGGGCCCCCTCTGCTCTCTGCTGGAGGCTGAGGCTCTG 1206
1358 TCCGTGCACTACTCCCGAAGCTCTGGGCCCCCTCTGCTCTCTGCTGGAGGCTGAGGCTCTG 1417
1207 CACTGCACTGCTCTCCAGGCGAGCCCGCCCCCTCTCTGCTCTGCTGGGCTGAGGCTCTG 1266
1418 CACTGCACTGCTCTCCAGGCGAGCCCGCCCCCTCTCTGCTCTGCTGGGCTGAGGCTCTG 1477
1267 GAGCTGCTGGAGGGGACAGCCAGGCTCTCTGAGGCTCAGCCCGAGCTCAGCCCGG 1326
1478 GAGCTGCTGGAGGGGACAGCCAGGCTCTCTGAGGCTCAGCCCGAGCTCAGCCCGG 1537
1327 CCCTGGGCGCAACAGCTCCCTGAGCTCCATGAGGCTCAGCTCCGCGCTCAGGCTCCCG 1386
1538 CCCTGGGCGCAACAGCTCCCTGAGCTCCATGAGGCTCAGCTCCGCGCTCAGGCTCCCG 1597
1387 TGTGAGGCTGGAAGCTCATATGAGGCGCCAGGAGTGCATCTGAGCTGCGGAGTAAG 1446
1598 TGTGAGGCTGGAAGCTCATATGAGGCGCCAGGAGTGCATCTGAGCTGCGGAGTAAG 1657
1447 AAGGAGTCACTCAAGCGCAATCTCAAGCGGAGCTTCTGGGAATCGGATCAGCGCT 1506
1658 AAGGAGTCACTCAAGCGCAATCTCAAGCGGAGCTTCTGGGAATCGGATCAGCGCT 1717
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1718 CTCTCTTCTCTGCTGGGCTGATCATCATGAAGATTTACCGAAGAGAGGACTCAG 1777
1567 ACAGAAACCCGAGGCGCAGGTTCTCCGCGCAGCAGGATCTGATTAATCAATGTG 1626
1778 ACAGAAACCCGAGGCGCAGGTTCTCCGCGCAGCAGGATCTGATTAATCAATGTG 1837
1627 GTCCGAGGCTGCGCCCTGCTCAGAGCGGAATCAGAAAGCCACACCAACAGTCT 1686
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1687 CGGAGCCCTCTTCCAGAGGCTCTCCCTCCCGAATCAAGAGAACCCAGAAAGAG 1746
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1747 TATCAGTTGCCAGTTTCCAGAACCCCAATCATCACTCAAGCCCCCAGAAATCCAGGAG 1806
1958 TATCAGTTGCCAGTTTCCAGAACCCCAATCATCACTCAAGCCCCCAGAAATCCAGGAG 2017
1807 AGCAGAGAGGCTCATATATGACGCTCACTTCCAGGGGCTCAGACCCAGGCTGAG 1866
2018 AGCAGAGAGGCTCATATATGACGCTCACTTCCAGGGGCTCAGACCCAGGCTGAG 2077
1867 GCCCGATGCCCAAGGCGACCCAGGCGGATATGACAGAGTCAAGTTCCAA 1917
2078 GCCCGATGCCCAAGGCGACCCAGGCGGATATGACAGAGTCAAGTTCCAA 2128

RESULT 7

US-09-984-130-148

Sequence 148, Application US/09984130

Publication No. US20030055231A1

GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 12 Human Secreted Proteins
FILE REFERENCE: PF489P2
CURRENT APPLICATION NUMBER: US/09/984,130
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/243,792
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 09/836,353
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR FILING DATE: 2000-04-19
PRIOR APPLICATION NUMBER: PCT/US99/25031
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR FILING DATE: 1998-10-28
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 148
LENGTH: 2338
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (3)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (6)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (9)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (11)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (12)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (17)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (18)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (21)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (23)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (25)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (26)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (27)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (28)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (29)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (30)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (31)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (32)

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 2121 TATCAGTTGCCAGTTTCCAGAAACCCAAATCATCCACTCAAGCCCCAGAAATCCAGAG 2180
 1807 AGCAGAGGAGCTCCATTATGACAGCTCAACTTCCAGCGGTACAGCCAGGCTTGG 1866
 2181 AGCAGAGGAGCTCCATTATGACAGCTCAACTTCCAGCGGTACAGCCAGGCTTGG 2240
 1857 GCCCGATGCCCAAGGACCCAGCGGATATGACAGAGTCAAGTTCCAA 1917
 2241 GCCCGATGCCCAAGGACCCAGCGGATATGACAGAGTCAAGTTCCAA 2291

RESULT 8

US-09-910-600-3

Sequence 3, Application US/09910600

Publication No. US2003036631A1

GENERAL INFORMATION:

APPLICANT: Longphre, Malinda

APPLICANT: Chang, Han

APPLICANT: Whitney, Gena

TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF

FILE REFERENCE: D0003NP

CURRENT APPLICATION NUMBER: US/09/910,600

CURRENT FILING DATE: 2001-07-20

PRIOR APPLICATION NUMBER: 60/220,139

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 2823

TYPE: DNA

ORGANISM: Homo sapiens

US-09-910-600-3

Query Match 78.1%; Score 1497.4; DB 10; Length 2823;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1498; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

419 CAGTGTCTCAGTTTACGCGCCAGACCCAGACCAACACCGACCTTACCTGCCATGTGG 478
 238 CAGTGTCTCAGTTTACGCGCCAGACCCAGACCAACACCGACCTTACCTGCCATGTGG 297
 479 ACTTCTCCAGAAAGGGTGTGAGGCGCACAGAGGACCGTCCGACTCCGTGTGGCTATGCC 538
 298 ACTTCTCCAGAAAGGGTGTGAGGCGTACAGAGGACCGTCCGACTCCGTGTGGCTATGCC 357
 539 CCAGAGACCTTGTATCAGCATTTACGTGACAAACAGCGCCCTGGAGCCGCCAGCC 598
 358 CCAGAGACCTTGTATCAGCATTTACGTGACAAACAGCGCCCTGGAGCCGCCAGCC 417
 599 AGGAAATGTCCATACCTCGAAGCCCAAAAGGCCAGTTTCTCGCGCTCCTGTGCTG 558
 418 AGGAAATGTCCATACCTCGAAGCCCAAAAGGCCAGTTTCTCGCGCTCCTGTGCTG 477
 659 CTGACGCCAGCCCTTCCACACTGAGCTGGTGGTCTCTGACAGACAGAGTCTCTCTCGT 718
 478 CTGACGCCAGCCCTTCCACACTGAGCTGGTGGTCTCTGACAGACAGAGTCTCTCTCGT 537
 719 CCTATCCTGGGCGCTTACAGCCCTGGGCTGAGCTGCCCGGGTGAAGGCTGGGATT 778
 538 CCTATCCTGGGCGCTTACAGCCCTGGGCTGAGCTGCCCGGGTGAAGGCTGGGATT 597
 779 CAGGCGCTACACTGCCCGAGCGGAGAAACAGGCTTGGCTCCAGCAGCAGGACCTGGACC 838
 598 CAGGCGCTACACTGCCCGAGCGGAGAAACAGGCTTGGCTCCAGCAGCAGGACCTGGACC 557
 839 TCTCTGTGAGTATCTCCAGAGAACTCTGAGTGTATGTTTCCMAGCAAAACAGACAG 898
 658 TCTCTGTGAGTATCTCCAGAGAACTCTGAGTGTATGTTTCCMAGCAAAACAGACAG 717
 899 TCTGTGAAACCTTGGAAACGGCACCTCTCTCCAGTACTGAGGCGCCAAAGCCTGTGCC 958

718 TCTGTGAAACCTTGGAAACGGCACCTCTCTCCAGTACTTGAGGCGCCAAAGCCTGTGCC 777
 959 TGGTCTGTGTACACACAGCAGCGCCCGCCAGCAGCTGAGCTGGAACCCAGAGGACAGG 1018
 778 TGGTCTGTGTACACACAGCAGCGCCCGCCAGCAGCTGAGCTGGAACCCAGAGGACAGG 837
 1019 TTTGAGAGCCCTTCCAGAGCCTCAGACCCCGGGGCTCTGAGAGCTGCTCGGGTTCAAGTGG 1078
 838 TTTGAGAGCCCTTCCAGAGCCTCAGACCCCGGGGCTCTGAGAGCTGCTCGGGTTCAAGTGG 897
 1079 AGCAGAGAGAGTTCAGCTGCCAGCTTGGGACACCCACTGGGCTTCCAGACAGTCTCTC 1138
 898 AGCAGAGAGAGTTCAGCTGCCAGCTTGGGACACCCACTGGGCTTCCAGACAGTCTCTC 957
 1139 TCAGGCTCTCCGTGCACTACTCCCGAAGCTCTCTGGGCGCCCTCTCTGCTCTCTGGAGGCTG 1198
 958 TCAGGCTCTCCGTGCACTACTCCCGAAGCTCTCTGGGCGCCCTCTCTCTCTGGAGGCTG 1017
 1199 AGGGTCTGCATGCACTGCTCTCTCCAGGCGCAGCCCGGCGCCCTCTCTGCGCTGGTGGC 1258
 1018 AGGGTCTGCATGCACTGCTCTCTCCAGGCGCAGCCCGGCGCCCTCTCTGCGCTGGTGGC 1077
 1259 TTTGGGAGGAGCTGCTGGAGGGGAAACAGCAGCAGCTCTCTCGAGGTACCCCGCAGCT 1318
 1078 TTTGGGAGGAGCTGCTGGAGGGGAAACAGCAGCAGCTCTCTCGAGGTACCCCGCAGCT 1137
 1319 CAGCCGGGCGCTGGGCGCAACAGCTCTCTGAGCTCTCATGAGGGGTCAAGCTCCGCGCTCA 1378
 1138 CAGCCGGGCGCTGGGCGCAACAGCTCTCTGAGCTCTCATGAGGGGTCAAGCTCCGCGCTCA 1197
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 1439 CAGATAAGAGGAGCTCATCTCAACGGCATTTCTCAACGGAGCGTTTCTGGGAATCGGCA 1498
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 1438 TCAATGTGGTCCGACCGGCTGGCCCGCTGAGTCTAGAGCGGAAATCAGAAAGCCACCAA 1497
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 1498 ACAGTCTCGAGCCCTCTTCCRCAGGCTGCTCCCTCCAGANTCAAGAGAACAGCA 1557
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 1799 CCCAGAGAGCCAGAGAGCTCCATTTATGCGAGCTCAACTTCCAGGGGTGAGACCCA 1858
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RESULT 9

US-09-910-600-1

Sequence 1, Application US/09910600

Publication No. US2003036631A1

GENERAL INFORMATION:

:	APPLICANT:	Longphre, Malinda
:	APPLICANT:	Chang, Han
:	APPLICANT:	Whitney, Gena
:	TITLE OF INVENTION:	NOVEL SIGLECS AND USES THEREOF
:	FILE REFERENCE:	D0003NP
:	CURRENT APPLICATION NUMBER:	US/09/910,600
:	CURRENT FILING DATE:	2001-07-20
:	PRIOR APPLICATION NUMBER:	60/220,139
:	PRIOR FILING DATE:	2000-07-21
:	NUMBER OF SEQ ID NOS:	32
:	SOFTWARE:	Patentin Ver. 2.0
:	SEQ ID NO 1	
:	LENGTH:	2565
:	TYPE:	DNA
:	ORGANISM:	Homo sapiens
:	US-09-910-600-1	
Query Match 69.7%; Score 1337; DB 10; Length 2565;		
Best Local Similarity 85.1%; Pred. No. 0;		
Matches 1632; Conservative 0; Mismatches 0; Indels 285; Gaps 1;		
Qy	1	ATGCTACTGCCACGTGCTCTCGTCTGGCGGGTCCTCAGGCTATGCATGGGAGA 60
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Qy	61	TTCTGGATACGAGTGCAAGTAAGTAGTGGCGAGGCGCTGTGCACTCTGTGCC 120
Dd	189	TTCTGGATACGAGTGCAAGTAAGTAGTGGCGAGGCGCTGTGCACTCTGTGCC 248
Qy	121	TGCTCTTTCTCTACCCCGCACAGACTGGACAGGCTACCCAGAGCTTATGGTACTGG 180
Dd	249	TGCTCTTTCTCTACCCCGCACAGACTGGACAGGCTACCCAGAGCTTATGGTACTGG 308
Qy	181	TTCAAAGCAGTGACTGAGACAACCAAGGCTGCTCTGTGGCCACAACACCAGAGTCGA 240
Dd	309	TTCAAAGCAGTGACTGAGACAACCAAGGCTGCTCTGTGGCCACAACACCAGAGTCGA 368
Qy	241	GAGGTGGAATGAGCACCCGGGGCGGATCCAGCTCACTGGGATCCGCCCAAGGGAAAC 300
Dd	369	GAGGTGGAATGAGCACCCGGGGCGGATCCAGCTCACTGGGATCCGCCCAAGGGAAAC 428
Qy	301	TGCTCTTTGGTGATCAGAGACGCGCAGATGCAAGTAGTACAGTACTTCTTTGGGTG 360
Dd	429	TGCTCTTTGGTGATCAGAGACGCGCAGATGCAAGTAGTACAGTACTTCTTTGGGTG 488
Qy	361	GAGAGAGAAGCTATGTGAGATATAATTTCATGACGATGGTTCCTTTCTAAGATACA 420
Dd	489	GAGAGAGAAGCTATGTGAGATATAATTTCATGACGATGGTTCCTTTCTAAGATACA 548
Qy	421	GTGCTCAGCTTCACGCCCAGACCCCAGAGACACCAACCGACTCACTGCGCATGTGAC 480
Dd	549	GTGCTCAGCTTCACGCCCAGACCCCAGAGACACCAACCGACTCACTGCGCATGTGAC 608
Qy	481	TTCTCAGAAAGGTGTGAGGCGCACAGAGGACCGTCCGATCCGTGTGGCTATGCCCCC 540
Dd	609	TTCTCAGAAAGGTGTGAGGCGCACAGAGGACCGTCCGATCCGTGTGGCTATGCCCCC 668
Qy	541	AGAGACCTTTGTTATCAGCATTTTCAGTGACAACCGCCAGCGCCTGGAGCCCCCAG 600
Dd	669	AGAGACCTTTGTTATCAGCATTTTCAGTGACAACCGCCAGCGCCTGGAGCCCCCAG 728
Qy	601	GGAATATGCCCATACCTGGAAGCCCAAAAAGGCCAGTTCTTCGGGCTCCTCTGTGCTGCT 660
Dd	729	GGAATATGCCCATACCTGGAAGCCCAAAAAGGCCAGTTCTTCGGGCTCCTCTGTGCTGCT 788
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Qy	721	CATCCTCGGGGCCCTAGACCCCTCGGGCTGGAGCTGCCCGGGTGAAGGCTCGGGATTCA 780
Dd	849	CATCCTCGGGGCCCTAGACCCCTCGGGCTGGAGCTGCCCGGGTGAAGGCTCGGGATTCA 908

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DB	909	GGGCGCTACACCTGCGGACCGGAGAACAGGCTTGGCTCCACGACGAGCGGCGCTGGACCTC	968
QY	841	TCGTGCACTATCCTCCAGAGAACCTGAGAGTATGTTTCCCAAGCAAAACAGGACAGTC	900
DB	969	TCGTGCACTATCCTCCAGAGAACCTGAGAGTATGTTTCCCAAGCAAAACAGGACAGTC	1028
QY	901	CTGGAAAACTTTGGGAAACGGGACGCTCTCTCCAGTACTGAGGGGCCAAAGCCTGTGCTCTG	960
DB	1029	CTGGAAAACTTTGGGAAACGGGACGCTCTCTCCAGTACTGAGGGGCCAAAGCCTGTGCTCTG	1088
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QY	1021	CTGAGCCCTCCAGGCCCTCAGACCCCGGGGCTCTGGAGCTGCCTCGGTTCAAGTGGAG	1080
DB	1149	CTGAGCCCTCCAGGCCCTCAGACCCCGGGGCTCTGGAGCTGCCTCGGTTCAAGTGGAG	1208
QY	1081	CAGAAAGGAGATTACCTGCGCACGCTCGGCAACCACTGGGTCCGACGACGCTCTCTC	1140
DB	1209	CAGAAAGGAGATTACCTGCGCACGCTCGGCAACCACTGGGTCCGACGACGCTCTCTC	1268
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QY	1201	GGTCTGCATGCGAGCTGCTCTCTCCAGGCCAGCCCCGGCCCCCTCTCTGCGCTGGTGGCTT	1260
DB	1285	GGTCTGCATGCGAGCTGCTCTCTCCAGGCCAGCCCCGGCCCCCTCTCTGCGCTGGTGGCTT	1284
QY	1261	GGGAGGAGCTGCTGGAGGGGAACAGCAGCCAGGACTCTCTTCGAGGTCACCCCCAGCTCA	1320
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QY	1321	GCCGGGCCCTGGGCAACAGCTCCCTGAGGCTCCATGGAGGGCTCAGTCCGSGCTCAGG	1380
DB	1285	GCCGGGCCCTGGGCAACAGCTCCCTGAGGCTCCATGGAGGGCTCAGTCCGSGCTCAGG	1284
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DB	1285	CTCCGCTGTGAGGCTTGGAAAGTCCATGGGGCCAGAGTGGATCCATCTCTGCAGCTGCCA	1284
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DB	1285	-ATAAGAAAGGACTCATCTCAACGGGATTTCTCAACGGAGCGTTTCTGGGAATCGGGATC	1343
QY	1501	ACGGCTCTTTTCTCTGCTGGCCCTCATCATATGAAGATTCTTACCGAAGAGACGG	1560
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DB	1584	AAGCAGTATCAGTTGGCCAGTTTCCAGAACCCMAATCATCTCAAGCCCCAGATCC	1643
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DB	1644	CAGGAGGCCAAGAGGAGCTCCATTATGCGACGCTCAACTTCCCGAGGCGTCAGACCCAGG	1703
QY	1861	CCTCAGGCCCGGATGCCCCAAGGGCACCCAGGGGATTATGCAAGGTCAACTTCAA	1917

DB 1704 CCTGAGGCCGATGCTCCACAGGACCCAGCGGATTATGCAAGTCAAGTTCCAA 1760

RESULT 10

US-09-978-295A-258
Sequence 258, Application US/09978295A
Patent No. US20020156006A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary R.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kluvin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

FILE REFERENCE: P2630PIC11

CURRENT APPLICATION NUMBER: US/09/978,295A

CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

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PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392

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1321 GCCGGCCCTGGGCCAACAGCTCTCCGTGAGCTCCATGAGGGCTCAAGTCGGGCTCAGG 1380
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1381 CTCGCTCTGAGGCTGGAACTGCACTGAGGGCCAGAGTGGATCCATCTCGACCTGCCA 1440
1202 ----- 1201
1441 GATAGAGGAGGACTCATCTCAACGGCATTTCTCAACGGAGGGTTTCTGGGAATCGGCATC 1500
1202 -ATAAGAAGGAGCTCATCTCAACGGCATTTCTCAACGGAGGGTTTCTGGGAATCGGCATC 1260
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RESULT 11

US-09-978-697-258

Sequence 258, Application US/09378697

Patent No. US20020169284A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;

APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tomas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085697

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Best Local Similarity 85.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches 2; Indels 285; Gaps 1;

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DB 166 TGCTCTTTCTCTACCCCGGACAGACTGAGCAGGGTCTACCCAGCTTATGGTACTGG 225
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QY 541 AGAGACCTTTGTTATCAGCATTTTCACTGACAAACAGCCAGCCCTGGAGCCCCAGCCCCAG 600
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; Sequence 258, Application US/09978192A
; Patent No. US20020177553A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
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; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/077632
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Godowski, Paul J.
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James,
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
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	Query Match	59.6%; Score 1333.8; DB 10; Length 2764;
	Best Local Similarity 85.0%; Pred. No. 0;	
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1201 GGTCTGCACTGCAGCTCTCTCTCCAGGCGAGCCCGGCCCTCTCTCTGGCTGGTGGCTT 1260
1202 ----- 1201
1261 GGGAGGAGAGTGTGGAGGGGAAACAGACGCGAGGATCTCTTGGAGGTACCCCGAGCTCA 1320
1202 ----- 1201
1321 GCCGGGCCCTGGGCAACAGCTCCCTGAGCTCTCCATGGAGGGCTCAGTCCGGCCTCAGG 1380
1202 ----- 1201

1381 CTCCGCTGTGAGGCTTGAAACGTCCATGGGCGCCAGAGTGGATCCATCTCTCAGCTGCCA 1440
1202 ----- 1201
1441 GATAAGAGGAGCTCATCTCAAGGCAATCTCCAAACGAGAGCTTTCTGGGAATCGGATC 1500
1202 -ATAAGAGGAGCTCATCTCAAGGCAATCTCCAAACGAGAGCTTTCTGGGAATCGGATC 1560
1501 ACGCTCTCTTTCTCTCTCTGCTGCGCTGATCATCATGAAGATTTCTACCGAGAGACGG 1560
1261 ACGCTCTCTTTCTCTCTCTGCTGCGCTGATCATCATGAAGATTTCTACCGAGAGACGG 1320
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1621 CCTGAGGCCCGGATGCTCCAAAGGCGACCCAGCGGATTTATGCAAGATCAAGTTCCAA 1677

Search completed: November 9, 2004, 02:38:52
Job time : 1363.51 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 07:56:39 ; Search time 8978.76 Seconds
(without alignments)
7780.028 Million cell updates/sec

Title: US-09-937-636-2

Perfect score: 1917

Sequence: 1 atgcactgcactgcctgct.....atgcgaagtcgaagtccaa 1917

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	828.4	43.2	876	5	BQ711946
2	798.8	41.7	910	5	EX324896
3	716.2	37.4	2017	3	AK042488 Mus muscu
4	635.8	33.2	3939	3	AK036698 Mus muscu
5	611.4	31.9	936	2	BF663289
6	505	26.3	505	5	EX283650
7	456.2	22.9	730	6	CB554607
8	438.4	22.9	667	6	CB554607
9	421	22.0	514	5	EX470328
10	413.8	21.6	850	7	CO557070
11	398	20.8	669	5	BU696122
12	355.8	18.6	1011	5	EX345667
13	348	18.2	810	7	CO554499
14	333	17.4	494	4	BI360326
15	329.8	17.2	580	1	AA764005
16	323.8	16.9	606	2	BB243404
17	302.6	15.8	530	2	BE235138
18	300.2	15.7	542	2	BE849876
19	293.6	15.3	510	4	BM483921
20	290.4	15.1	520	5	EX526836
21	288.4	15.0	519	1	AI592207
22	288.4	15.0	1099	4	BM544297
23	288.4	15.0	1745	4	BM906520
24	285.8	14.9	483	1	AA162826

25	285.6	14.9	805	4	BI913042
26	285.2	14.9	1464	4	BM544269
27	272.2	14.2	871	4	BI518708
28	272.2	14.2	1714	3	BC030222
29	267	13.9	594	5	BU101663
30	265.2	13.9	2478	3	AK087658
31	263.6	13.8	617	7	CN789989
32	262.2	13.7	382	4	BM483922
33	260	13.6	769	7	CO565732
34	250	13.0	558	8	AQ533306
35	241.8	12.6	797	4	BI756629
36	226.8	11.8	628	7	CN369198
37	218.6	11.4	531	5	BI153418
38	215.2	11.2	828	7	CK600093
39	210.4	11.0	381	5	BY526658
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42	187.4	9.8	299	9	CE060061
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44	182.2	9.5	348	1	AA672534
45	177	9.2	1001	4	BM561814

ALIGNMENTS

RESULT 1
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LOCUS BQ711946
DEFINITION AGENCOURT_7977108 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215765
5', mRNA sequence.
ACCESSION BQ711946
VERSION BQ711946.1 GI:21850845
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

876 bp mRNA linear EST 16-JUL-2002
AGENCOURT_7977108 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215765
5', mRNA sequence.

REFERENCE 1 (bases 1 to 876)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCM2385 row: d column: 06

High quality sequence stop: 685.

Location/Qualifiers

1..876

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clones="IMAGE:6215765"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_113"

/note="Organ: spleen; Vector: pORF7; Site: 1; XhoI; Site 2:

EcoRI; CDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCACGAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH_MGC Library."

ORIGIN

Query Match 43.2%; Score 828.4; DB 5; Length 876;
Best Local Similarity 98.3%; Pred. No. 1.6e-196;

QY	1049	GGGCTCTGGAGCTGCTCGGGTTCAAGTGGAGCAGGAGAGATTACCTGCCACGCTC	1108
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QY	1109	GGCACCCACCTGGGCTCCACGACGCTCTCTCTCAGCCCTCTCCGTGCATCTACTCTCCCGGAAGC	1168
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QY	1169	TGCTGGGCCCCCTCTCTGCTCTGGAGGCTGAGGGTCTGCGCTGAGAGCTGCTCTCCAGG	1228
Db	655	TGCTGGGCCCCCTCTCTGCTCTGGAGGCTGAGGGTCTGCGCTGAGAGCTGCTCTCCAGG	714
QY	1229	CCAGCCCGGCCCTCTCTCTGCTGCTGGTGTGGGAGGAGCTGCTGGAGGGGAAACAGCA	1288
Db	715	CCAGCCCGGCCCTCTCTCTGCTGCTGGTGTGGGAGGAGCTGCTGGAGGGGAAACAGCA	774
QY	1289	GCCAGGACTCCTTTGAGGTCACCCAGCTCAGCCGGGCCCTGGGCGAAACAGCTCCCTGA	1348
Db	775	GTGAGGCTCTTTGAGGTCACCCAGCTCAGCCGGGCCCTGGGCGAAACAGCTCCCTGA	834
QY	1349	GCTTCATGAGGCTCAGCTCCGGCTCAGGCTCCGCTGAGGCTGGAAAGTCCATG	1408
Db	835	GTCTTCATGAGGCTCAGCTCAGGCTCAGGCTCCGCTGAGGCTGGAAAGTCCACC	894
QY	1409	GGGCCCCAGAGTGGATC	1424
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AK042488			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
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Db      3579 GCTGCTCTCACTTCTCCCGCTGAGAC---TGAGGAGACCCAGGATCCCCAGACACC 3635
Qy      1888 CAGCGGATTATGCAAGAGTCAAGTTCCA 1916
Db      3636 TATTCTGATTACACAGAGGTGAGAGTCCA 3664

RESULT 5
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LOCUS      60214414F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297851 5',
mRNA sequence.
ACCESSION  BF663289.1 GI:11937171
VERSION      BF663289.1
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 936)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI152 row: k column: 04
High quality sequence stop: 661.
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                     /lab_hosts="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /notes="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
                     Site 2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCAAGAG(G). Size-selected by Ling
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."

ORIGIN
Query Match      31.98; Score 611.4; DB 2; Length 936;
Best Local Similarity 95.48; Pred No. 4.5e-142;
Matches 705; Conservative 0; Mismatches 26; Indels 8; Gaps 7;

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Qy      894 GACAGTCCTGGAACCTTGGGAACGCGCTCTCTCCAGTACTGAGGGCCAAAGCCT 953
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Qy      954 GTGCCTGGTCTGTGTACACACAGACGACCCGCCAGCCAGGCTGAGCTGGACCCAGAGGGG 1013
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Qy      1194 GCTGAGGGTCTGCACTGCACTGCTCTCCAGGCGAGCCCGGCCCTCTCTGCGGTG 1253
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Qy      1553 AGAGACGAGCTCAGACAGA 1571
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DEFINITION BX283650.1 GI:28848104
ACCESSION  BX283650
VERSION     BX283650
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 505)
Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
Radelof,U., Schneider,D. and Korn,B.
Human Unigeneset - RZPD3
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGE:4297851;
RZPD; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPD LIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showlib.pl.cgi?response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
PCMW-M13u, Primer sequence: CGTTGTAAACAGCGCCAGT.
Location/Qualifiers
FEATURES

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736 AGACCCCTGGGCTGGAGCTGCCCGGGGTGAGGCTGGGATTTCAGGCGCTACACTGC 795
108 AGACCCCTGGGCTGGAGCTGCCCGGGGTGAGGCTGGGATTTCAGGCGCTACACTGC 49
796 CGAGCGGAGAACAGCGCTGGCTGCCAGCAGGAGCGCCCTGGACCTCTC 842
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CB554607 667 bp mRNA linear EST 01-JUN-2003
MSP0040_D05 WMSP Macaca mulatta cDNA, mRNA sequence.
CB554607_1 GI:31303802
EST.
Macaca mulatta (rhesus monkey)
Macaca mulatta
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
Cercopithecinæ; Macaca.
1 (bases 1 to 667)
Katze,M.G., Humbergarner,R., Korth,M., Feldman,R., Amjadi,M. and
Holzman,T.
Expressed sequence tags from Rhesus macaque spleen
Unpublished (2002)
Contact: Holzman T
Katze Lab
University of Washington
Box 358070, Seattle, WA 98195-8070, USA
Tel: 206 732 6156
Fax: 206 732 6055
Email: ted@locke.hs.washington.edu
Similar to GenBank entry AF311905 AF311905 Homo sapiens sialic
acid-binding Ig-like lectin 10 (SIGLEC10) mRNA, complete cds.
8/2001
Plate: MSP0040 row: D column: 05.

FEATURES             source
    Location/Qualifiers
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            /note="Organ: spleen"

ORIGIN
Query Match      22.9%; Score 438.4; DB 6; Length 667;
Best Local Similarity 94.2; Pred. No. 1.1e-98;
Matches 467; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

QY 1425 CATCTCGAGTGCAGATGAAGGAGCTCATCTCAAGCGCATTTCTCCACGAGCGTT 1484
Db 39 CAGCTTCTCGTGCACTATGAAGAGGACTCATCTCAAGCGCATTTCTCCACGAGCGTT 98
QY 1485 TCTGGGAATCGGCATCAGCGCTCTTTCTTCTCTGCTGCGCCCTGATCATCATGAAGAT 1544
Db 99 TCTGGGAATCGGCATCAGCGCTCTTTCTTCTCTGCTGCGCCCTGATCATCATGAAGAT 158
QY 1545 TCTACCGAGAGAGCGGACTCAGACAGAACCCGAGCCCGAGTTCTCCCGGCACAGCAC 1604
Db 159 TCTACCGAGAGAGAGACTCAGGACAGATACCCCAAGCCCGAGTTCTCCCGGCACAGCAC 218
QY 1605 GATCCTGGATTACATCAATGTGTCCGACGGGTGGCCCGCTGGCTCAGAACGGGAATCA 1664
Db 219 GATCCTGGATTACATCAATGTGTCCGACGGGTGGCCCGCTGGCTCAGAACGGGAATCA 278
QY 1665 GAAAGCCACACCAACAGATC---CTGGACCCCTCTTCCACAGAGTGTGCTCTCCCTCCCCAGA 1721
Db 279 GAAAGCCACACCAACAGATCTTCTTCTCGGACCCCTCTTCCACAGAGTGTGCTCTCCCTCCCCAGA 338

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QY 1722 ATCAAGAGAACACGAGAAAGACAGTATCAGTGTCCAGTTTCCAGAACCAATCATC 1781
Db 339 ATCAAGAGAACACGAGAAAGACAGTATCAGTGTCCAGTTTCCAGAACCAATCATC 398
QY 1782 CACTCAAGCCCGCAGAAATCCAGGAGAGCAAGAGGAGCTCCATTATGCGACGCTCAACTT 1841
Db 399 CACTCAAGCCCGCAGAAATCCAGGAGAGCAAGAGGAGCTCCATTATGCGACGCTCAACTT 458
QY 1842 CCCAGGCGTCAGACCCAGGCGCTGAGCGCCGAGTCCCAAGGCGACCCAGGCGGATTATGC 1901
Db 459 CCCAGGCGTCAGACCCAGGCGCTGAGCGCCGAGTCCCAAGGCGACCCAGGCGGATTATGC 518
QY 1902 AGAAGTCAAGTTTCCAA 1917
Db 519 AGAAGTCAAGTTTCCAA 534

RESULT 9
BX470328 514 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZp779N169_r1.779 (synonym: hnccl) Homo sapiens cDNA clone
DEFINITION DKFZp779N169 5', mRNA sequence.
ACCESSION BX470328
VERSION BX470328.1 GI:32023094
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 514)
Bloeker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
Fobo,G., Han,M. and Wiemann,S.
EST (Bioecker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., et al.)
Unpublished (2003)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GSF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No si sequence available.
This clone (DKFZp779N169) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES             source
    Location/Qualifiers
        1..514
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            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="DKFZp779N169"
            /tissue_type="liver"
            /dev_stage="fetal"
            /lab_host="DH10B"
            /clone_lib="779 (synonym: hnccl)"
            /note="Vector: pSport1_sfi; Site_1: sfiA; Site_2: sfiB"

ORIGIN
Query Match      22.0%; Score 421; DB 5; Length 514;
Best Local Similarity 97.7%; Pred. No. 2.3e-94;
Matches 427; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ATGTACTGCCACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
Db 63 ATGTACTGCCACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 122
QY 61 TTCTGGATACAGTGCAGGAGTCAAGTGTGTCGGAGGCGCTGTGCATCTCTGTGCC 120
Db 123 TTCTGGATACAGTGCAGGAGTCAAGTGTGTCGGAGGCGCTGTGCATCTCTGTGCC 182

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121 TGCTCTTTCTCTACCCGACCAAGACTGGACAGGCTCTACCCAGCTTATGGCTACTGG 180
Db TGCTCTTTCTCTACCCGACCAAGACTGGACAGGCTCTACCCAGCTTATGGCTACTGG 242
Qy TTCAAGAGCTGACTGAGACCAACCAAGGCTCTCTGGGCCACCAACACAGAGTGA 240
Db TTCAAGAGCTGACTGAGACCAACCAAGGCTCTCTGGGCCACCAACACAGAGTGA 302
Qy GAGGTGGAATGAGCACCAGGCGGCGGATTCACAGCTCACTGGGATCCCGCCAGGGGAAC 300
Db GAGGTGGAATGAGCACCAGGCGGCGGATTCACAGCTCACTGGGATCCCGCCAGGGGAAC 362
Qy TGCTCTTTCTCTACCCGACCAAGACTGGACAGGCTCTACCCAGCTTATGGCTACTGG 360
Db TGCTCTTTCTCTACCCGACCAAGACTGGACAGGCTCTACCCAGCTTATGGCTACTGG 422
Qy GAGGTGGAATGAGCACCAGGCGGCGGATTCACAGCTCACTGGGATCCCGCCAGGGGAAC 420
Db GAGGTGGAATGAGCACCAGGCGGCGGATTCACAGCTCACTGGGATCCCGCCAGGGGAAC 482
Qy GTGCTGAGTTCAGGCC 437
Db GCCTGACTCAGAAGCC 499

RESULT 10
COS57070
LOCUS
DEFINITION
AGENCOURT_28539076 NIH_MGC_249 Rattus norvegicus cDNA clone
IMAGE:7376699 5', mRNA sequence.
COS57070
COS57070.1 GI:50369433
EST.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 850)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cga@nci.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
College of Wisconsin
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM15529 row: d column: 09
High quality sequence stop: 665.
Location/Qualifiers
1..850
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/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7376699"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_249"
/note="Organ: spleen; Vector: pExpress-1; Site 1: EcoRV;
Site 2: NotI; RNA obtained from testis tissue of 8 wk old
animal. Tissues were snap-frozen and kept at -80C before
RNA extraction and purification (TRI-reagent method). cDNA
was primed using oligo-dT primer:
5'-pGACTGTTCTAGTCGAGCGGCCGCC(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb
resulted in an average insert size of 1.4 kb. This primary

FEATURES
source
1..850
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7376699"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_249"
/note="Organ: spleen; Vector: pExpress-1; Site 1: EcoRV;
Site 2: NotI; RNA obtained from testis tissue of 8 wk old
animal. Tissues were snap-frozen and kept at -80C before
RNA extraction and purification (TRI-reagent method). cDNA
was primed using oligo-dT primer:
5'-pGACTGTTCTAGTCGAGCGGCCGCC(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb
resulted in an average insert size of 1.4 kb. This primary

library is normalized (primary library is NIH_MGC_248)
and was constructed by Express Genomics (Frederick, MD).
Note: this is a NIH_MGC library"

Query Match 21.6%; Score 413.8; DB 7; Length 850;
Best Local Similarity 77.1%; Pred. No. 1.7e-92;
Matches 516; Conservative 0; Mismatches 152; Indels 1; Gaps 1;

Qy 589 CCCAGCCCCAGGGAATGTCTCCATACCTGGAAGCCCAAGGCGGCTCTCTAGCTCTC 648
Db 16 CCAGAACTGAATAGGAATCCTTCACTCTGGAAGTTCAACAAAGGCGGCTCTCTAGCTCTC 75
Qy 649 CTCCTGCTGTGACAGCAGGCGGCTCTCCACACCTGAGTGGTCTCTGCAACAGAGTCT 708
Db 76 CTCCTGCTGTGACAGCAGGCGGCTCTCCACACCTGAGTGGTCTCTGCAACAGAGTCT 135
Qy 709 CTCCTGCTGTGACAGCAGGCGGCTCTCCACACCTGAGTGGTCTCTGCAACAGAGTCT 768
Db 136 CTCCTGCTGTGACAGCAGGCGGCTCTCCACACCTGAGTGGTCTCTGCAACAGAGTCT 195
Qy 769 GCTGGGGAATTCAGGCGGCTCTACCTGCGGAGGAGAACAGGCTTGGTCTCCAGCAGGA 828
Db 196 GCTGGGGAATTCAGGCGGCTCTACCTGCGGAGGAGAACAGGCTTGGTCTCCAGCAGGA 255
Qy 829 GCTGGGGAATTCAGGCGGCTCTACCTGCGGAGGAGAACAGGCTTGGTCTCCAGCAGGA 888
Db 256 GCTGGGGAATTCAGGCGGCTCTACCTGCGGAGGAGAACAGGCTTGGTCTCCAGCAGGA 315
Qy 889 AACAGGAGCTCTGGGAAACCTTGGGAAACCTTGGGAAACCTTGGGAAACCTTGGGAA 948
Db 316 AACAGGAGCTCTGGGAAACCTTGGGAAACCTTGGGAAACCTTGGGAAACCTTGGGAA 375
Qy 949 AGCTGTGCTGCTGTGTCACACAGCAGGCGGCGGCTCTGAGTGGTCTCTGAGTGGTCT 1008
Db 376 AGCTGTGCTGCTGTGTCACACAGCAGGCGGCGGCTCTGAGTGGTCTCTGAGTGGTCT 435
Qy 1009 AGCTGTGCTGCTGTGTCACACAGCAGGCGGCGGCTCTGAGTGGTCTCTGAGTGGTCT 1068
Db 436 AGCTGTGCTGCTGTGTCACACAGCAGGCGGCGGCTCTGAGTGGTCTCTGAGTGGTCT 495
Qy 1069 GTTCAAGTGGAGCAGCAAGGAGAGTTCACCTGCCAGCTCGCACCCAGCTGGTCTCCAG 1128
Db 496 GTTCAAGTGGAGCAGCAAGGAGAGTTCACCTGCCAGCTCGCACCCAGCTGGTCTCCAG 555
Qy 1129 CAGCTCTCTCAGGCTCTCGTGGCTCTCTGTCAGTCTCCCGAGGCTCTGGGCTCTCT 1188
Db 556 CAGCTCTCTCAGGCTCTCGTGGCTCTCTGTCAGTCTCCCGAGGCTCTGGGCTCTCT 615
Qy 1189 TGGAGGCTGAGGCTCTGTCAGTCTCTCTCCAGGCGGCTCTCTCCAGGCGGCTCTCT 1248
Db 616 TGGAGGCTGAGGCTCTGTCAGTCTCTCTCCAGGCGGCTCTCTCCAGGCGGCTCTCT 674
Qy 1249 CGCTGGTGG 1257
Db 675 CGCTGGG 683

RESULT 11
BU696122
LOCUS
DEFINITION
LL2in12696T7 Hematopoietic Stem Cell Subtracted Library Mus
musculus cDNA 5' similar to OB binding proteins, mRNA sequence.
ACCESSION
BU696122
VERSION
BU696122.1 GI:23604852
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 669)
REFERENCE
Phillips, R.L., Bruns, R.E., Brunk, B.P., Ivanova, N., Mahan, M.A.,
Deanehan, J.K., Moore, K.A., Overton, G.C. and Lemischka, I.R.


```
Qy 62 TCTGATACAGTSCAGAGTCAAGTATGG-TGCCGAGGGCCCTGTGTCATCTCTGTGCC 120
Db 93 AAGTCTTCAAGTSCAGAGGAGGTGCGCGNTGCCGAGGCGCTGTGTGTCATCGTGTCT 152
Qy 121 TCTCTTTTCTCTACCCCGGACAGAGTGCAGAGGTCTACCCAGCTTATGCTACTGG 180
Db 153 TGCACCTCTCTCTACCCCGGAGTGGTGGGAGAGTCTACTCTGTGTATGCTACTGG 212
Qy 181 TTCAAAGCAGTACTGAGACAACCAAGGGTCTCTCTGTGGCCCAAAACCAACAGAGTCGA 240
Db 213 TTCAAAGCAGGACCCCAAGACCGGTCTCTGTGGCCACTAACACAGAGTCGA 272
Qy 241 GAGTGAATGAGACCCGGGGCCGATTCAGCTCTCTGGGATCCCGCAAGGGGAAC 300
Db 273 GAGTGAATGAGACCCGGGACCGATTCAGCTCTCTGGGATCCCGCAAGGGGAGC 332
Qy 301 TGCTCTTGTGTATCAGAGAGCGCAGATGCAGATGAGTCAGTACTTCTTTCGGTG 360
Db 333 TGCTCTTGTGTATCAGAGAGCGCAGAGGAGATGAGCATGTACTTCTTTCGGTG 392
Qy 361 GAGAGAGAGTATGTGAGATATAATTTTCATGAACGATGGTCTTCTTAAAGTAA-- 418
Db 393 GAGAGAGAGCGGTGTGAGACATAGTTTCTGAGCAATCGTCTTCTTAAAGTAA 452
Qy 419 ----- 418
Db 453 GCCCTGACTAAGAGCCTGATGTCTATCCCGAGACCTGGAGCCCGGCGACCGGTG 512
Qy 419 ----- 418
Db 513 ACGTCTATCTGTGTGTTTAACTGGGCTTCAAGAAATGTCCAGCCCTCTTCTCTCTGG 572
Qy 419 ----- 418
Db 573 ACGGGGCTGCCCTCTCCCTAGAAAGAACAGACCAAGACCTCCCACTTCTCAGTGCTC 632
Qy 427 AGCTTTCACGCCAGACCCAGGACCAACACACGACCTCACCTGCCATGGACTTCTCC 486
Db 633 AGCTTTCACGCCAGACCCAGGACCAACACGACCTCACCTGCCATGGACTTCTCC 692
Qy 487 AGAAAGGTTGACGCGACAGAGAGCGTCCGACTCGTGTGGCTATGCCCCAGAGAC 546
Db 693 AGAAAGGTTGACGCGACAGAGAGCGTCCGACTCGTGTGGCTATG-CCCCAAAGAC 751
Qy 547 CTTGTTATCAGCATTTTACCTGACACACCGCCGCTGGAGCCCGAGCCCGAGGGAAT 606
Db 752 CTTATTATCAGCATTTTACATGACACACGCTGAGCCCTGGAAT-CCCCAGGGAAC 805
Qy 607 GTCCCATACCTGGAAGCCCAAGAGCCAGTCTCTGCGGCTCTCTGTGTGTGCTGACAGC 666
Db 806 GTCATATATCTGGAAGTTCAGAAAGCCAGTCTCTGCGGCTCTCTGTGTGTGCTGACAGC 865
Qy 667 CAGCCCTGTCACACTGAGCTGGGTCTGAGAAACAGAGTCTCTCTGTCGTCATGCC 726
Db 866 CAGCCCTGTCGCGGCTGAGCTGGGTCTGAG-GCAGAGTCTCTCTGTCGTCATGCC 924
Qy 727 TGGGGCTTACAGCCCTGGGCTGAGAGCTGCGGGGTGAAGGCTGGGGATTCAGGGCGC 786
Db 925 TRGGSCMCMGAAACCTTGGGGTGCAGTCTGGTGGGTACGGGGGGGATTTAMGGGCGAC 984
Qy 787 TACACCTGCCGAG 799
Db 985 MCYTGCGASSGAG 997
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RESULT 13
CO555499 LOCUS
DEFINITION CO555499 810 bp mRNA linear EST 19-JUL-2004
AGENCOURT 28542322 NIH_MGC_249 Rattus norvegicus cdna clone
IMAGE:7375918 5', mRNA sequence.
ACCESSION CO555499
VERSION CO555499.1 GI:50367692
KEYWORDS EST.
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SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 810)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
BiG. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
College of Wisconsin
CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM1527 row: c column: 20
High quality sequence stop: 632.
Location/Qualifiers
1. 810
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/clone="IMAGE:7375918"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_249"
/note="Organ: spleen; Vector: pExpress-1; Site: 1: EcoRV;
Site 2: NotI; RNA obtained from testis tissue of 8 wk old
animal. Tissues were snap-frozen and kept at -80C before
RNA extraction and purification (Tri-reagent method). cDNA
was primed using oligo-dT primer:
5'-GACTAGTCTAGATCGAGCGCGCC(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size selection >1.25kb
resulted in an average insert size of 1.4 kb. This primary
library is normalized (primary library is NIH_MGC_248)
and was constructed by Express Genomics (Frederick, MD).
Note: this is a NIH_MGC library"

FEATURES
source

Query Match 18.2%; Score 348; DB 7; Length 810;
Best Local Similarity 71.3%; Pred. No. 5.4e-76;
Matches 506; Conservative 0; Mismatches 190; Indels 14; Gaps 3;
Qy 1094 TCACCTGCCACGCTCGGCACCCACCTGGCTCCAGCAGTCTCTCTCAGCCCTCCGTGC 1153
Db 1 TCACCTGTGCTGCACAGAGCCACCTGGGCACCCAGCGCATCTCTGAGCCCTCTGTGTC 60
Qy 1154 ACTATCCCGAAGTGTGTGGCCCTCTCTGTCTCTGGAGGCTGAGGTTGCACTGCA 1213
Db 61 ACTACCCACCCAGATGTCAGACCCCTCTGCTCTGGGATTTCTGAGGTTCTGCACTGCA 120
Qy 1214 GCTGTCTCTCCAGAGCCAGCCCGGCCCTCTCTCGCTGTGTGGCTGGGAGGAGCTGC 1273
Db 121 GCTGTCTCTCCAGAGCCCTGGCTGCCCCCTCTTTCGCTGCGGCTGGGAGGAGGCTGC 180
Qy 1274 TGGAGGGAAACAGCAGGAGGACTCTCTTCGAGGTCAACCCAGCTCAGCCCGGCGCTGG 1333
Db 181 TGGAGGGAAACAGCAGGAGGACTCTCTTCAAGTCAACCTCCAGCTCACTTGGACCTGG 240
Qy 1334 CCAACAGCTCCCTGAGCTCCATGGAGGCTCAGTCCGGCTCAGGCTCCGCTGTGAGG 1393
Db 241 CCAACAGCTCCCTGAGCTCCCTTTCAGGAGCTGGAACCCAGGCTCTGGCTCAGCTGTGAG 300
Qy 1394 CTTGGAAGCTCCATGGGGCCAGAGTGGATTCATCTCTGAGCTGCCAGATAGAGAGGAC 1453
Db 301 CTTGGAACCCATGGGGCCAGAGACCTCTCTGCTCTCTGCTACCTGATAAAA- 355

ORIGIN

35	1454	TCATCTCAACGGGATTTCTCAACGGAGCGTTTCTGGGAATCGGCATCACGGCTCTCTCTTT	1513
36			
37			
38	356	-CAGTTCCGGAGCATTTCTCAAGGGAGCAGCTTTGGGCTTTGGCATTTACAGCCCTCCTTG	414
39			
40	1514	TCCTCTCCCTGGCCCTGATCATCATGAAGATTCTACCGAAGAGACGGACTCAGACAGAAA	1573
41			
42	415	CCCTCTGCCTCGTCGTGATCATCATGAAGACCCTACAGAAGAAAGGAACCCAGAGGTAA	474
43			
44	1574	CCCGAGGCCGACAGTTCTCCGGGACAGCAGCATCTCHGGATTACATCAATGTGGTCCCGA	1633
45			
46	475	CCTCAAGGCCCAAAATCTCAGGGGACAGCAATCTCTGGATTACATCAATGTGGTCCCGCA	534
47			
48	1634	CGGCTGCCGCCCTTGGCTCTAGAAGCGGAATCAGAAAGGCCACACCAAAACAGTCTCTGGACCC	1693
49			
50	535	AGACCAAGTCCCGGCT-----CGGAATTTGAAAGCTGAACACAGACACCCCTCTGGGA	588
51			
52	1694	CTCTTCCACAGGTGTCCTCTCCCGAGATTAAGAGAGACCGAGAAAACGAGTATCAGT	1753
53			
54	589	TTTGGCCCCCTGGACACTCATCTCCCTTAAGCAA--GAAGAGCAGAGGACCAAGTTTTCA	646
55			
56	1754	TGCCAGTTTCCAGAACCCAAATCATCTCAACTCAAGCCCCCAGATCCAG	1803
57			
58	647	TCCCTGTTTCCAGACCCAGACATCTCTCGGCCCATCTCTTAATAACAG	696
59			

Query Match

17.4%; Score 333; DB 4; Length 494;

		Best Local Similarity	80.4%; Pred: No.	2.8e-72;	Matches	390; Conservative	0; Mismatches	95; Indels	0; Gaps	0;
QY	724	CCTCGGGGCCCAGACCCCTTGGGGGTGGAGCTTCGCCGGGGTGGAAGCCTGGGGATTCAAGGG	783							
Dd	10	CGCTCACGCTCCAGAACCCTTTGCAGCTGGTGTCTGCCCTGGTGAAGGCTGAGGATCGGGC	69							
QY	784	CGCTACACTGCCGAGCGAGAACAGGCTTGGCTCCAGACAGGAGCCTTGACCTCTCT	843							
Dd	70	CGCTACACTTGAGAGCAGAGAAACAGGTTAGGCTCTGAGAGCGGAGCCTGGACCTTTCT	129							
QY	844	GTCGAGTAFTCTCCAGAGAACCTTGAGAGTGGTTTTCCCCAAGCAAACAAGCAGAGTCCTG	903							
Dd	130	GTGCGATAFGCCCCAGAGAACCTGAGAGTGGCTCTCCAAGCAAATAGGACAGTCTCTG	189							
QY	904	GAAAACCTTGGAAACGGGACGTCTCTCCAGTAGTCTGGAGGGCCRAAGCCTGTGCCCTGTC	963							
Dd	190	GAAAGCTTCGGGAAATGCAATCATCCATCCCGGTCCTGGAGGGCCAAAGCCTGGCTCTACTC	249							
QY	964	TGTGTACACACAGCAGCCCCCGCCAGCGCTGAGCTGGACCCAGAGGGGACAGGTTCTG	1023							
Dd	250	TGTGTCACTCACAGCAACCCCGACGCCAGCTGAGTGGACCCGAGCGGACAGACTCTG	309							
QY	1024	AGCCCTCTCCAGCGCTTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCAGTGGAGCAC	1083							
Dd	310	GGCCCTCTCCAGCTCTCAGACTCTGGGGTCTCTGGAACTSCCTCAGATACAAAAAGAACAG	369							
QY	1084	GAGGAGAGTTCACTGCGCACCTGGGACCCACACATGGGCTCCAGCAGCTCTCTCTCAGC	1143							
Dd	370	GAAAGAGAAATCACCTGTCTGGGCTTCAAGAACCGCTGGGCTCCAGAACTCTCTCTGAGC	429							
QY	1144	CTCTCGGTGCACACTCTCCCGGAAGCTGTGGGCCCTCTCTCTCTGGAGGCTCAGGCT	1203							
Dd	430	CTCTTGGTGGGTACTCCCCCGCCAGCTGTGGGTCTCTCTCTCTGGAGGACGGGT	489							
QY	1204	CTGCA	1208							
Dd	490	CTCCA	494							
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RESULT	15									
LOCUS	AA764005									
DEFINITION	vM3Dn02.r1 Soares_thymus_2BndMt Mus musculus cDNA clone IMAGE:1243299 5' similar to SM:MAGE_MOUSE P16880 MYELIN-ASSOCIATED GLYCOPROTEIN, SHORT FORM PRECURSOR ; , mRNA sequence.									
ACCESSION	AA764005									
VERSION	AA764005.1 GI:2811527									
KEYWORDS	EST.									
SOURCE	Mus musculus ('house mouse')									
ORGANISM	Mus musculus									
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 580)									
AUTHORS	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubouque,T., Geisel,S., Kucaba,T., Lacy,M., Le.M., Martin,J., Morris,M., Schellenberg,K., Steptos,M., Tan,F., Underwood.K., Moore.B., Threlsing,B., Wylie,I., Lennon,G., Soares,B., Wilson,R. and Waterston.R.									
TITLE	The WashU-HHMI Mouse EST Project									
JOURNAL	Unpublished (1996)									
COMMENT	Contact: Marra M/Mouse EST project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: museest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGJ:656987 Seq primer: -28ml3 rev2 ET from Amershams High quality sequence stop: 503.									

FEATURES
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1. .580
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/db_xref="taxon:10090"
/clone="IMAGE:1243299"
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/lab_host="DH10B"
/clone_lib="Soares thymus_2NDMT"
/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5,
TGTTACAACTCAAGTGGAGCGCGGTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p773 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 17.2%; Score 329.8; DB 1; Length 580;
Best Local Similarity 75.0%; Pred. No. 1.9e-71;
Matches 428; Conservative 0; Mismatches 137; Indels 6; Gaps 1;
QY 523 CGTGTGGCCCTATGCCCGCAGAGACCTTGTTATCAGCATTTTCAGTGACACAGCGCCAGCC 582
Db 16 CTTCTCCCGAGTGCCTCCAGATCTCTTGCTATCAGCATTTTCATGACAAATGTATCAGTC 75
QY 583 CTGGAGCCCGCAGCCCGCAGGGAATGTCCTATCTGGAAGCCCAAAAGGCCAGTTCCTG 642
Db 76 -----CCAGACTTGCATGAGAATCCTTCACATCTGGAAGTTCAGCAAGGCCAGTCTCTT 129
QY 643 CGGCTCCTCTGCTGCTGACACGACGCCCTGCGCACACTGAGCTGGGTCTGCGAGAC 702
Db 130 CGCCTCCTCTGCTGCTGACACGACGCCCTGCTACACTGAGCTGGGTCTGAGGAC 189
QY 703 AGAGTCTCTCTCTGCTGCCATCCTCGGGCCCTAGACCCCTGGGGGTGGAGCTGCCCGGG 762
Db 190 CAAGTCTCTTTCTGGTCTAGCCCTGTGGGTGCGAAGCCCTGSCACTAGAGCTGCCCTGG 249
QY 763 GTGAAGCTGGGATTCAGGGCCCTACACTGCGGAGCGGAGAACAGGCTTGGCTCCCGAG 822
Db 250 GTGAAAGCTGGGACTCTGGACACTACACTGCCAAGCAGAGAATAGGCTGGGCTCCCGAG 309
QY 823 CAGCGAGCCCTGGACCTCTCTGTGCAGTATCTCCAGAGAACCTCCAGAGTGTATGGTTTCC 882
Db 310 CAACATACCTTGACCTCTCTGTGCTGTACCCCTCCAGACCTGAGAGTACTGTCTTCC 369
QY 883 CAAGCAACAGGACAGTCTCTGGAACCTTTGGGAACGGCACGTCCTCCCACTACTGGAG 942
Db 370 CAAGCAACAGGACAGTGTGTGAAATCCTCAGGAATGCCATCTCCCTCCCGCTCTGGAG 429
QY 943 GGCCTAAGCTGTGCTGTGCTGTGTCACACAGCAGAGCCCGCCAGCCAGGCTGAGCTGG 1002
Db 430 GGCCTAAGCTGTGCTGTGCTGTGTCACCTATAGCAATCCCCCAGCCCAATGTAGTTGG 489
QY 1003 ACCCAGAGGGGACAGTTCCTGAGCCCTCCAGCCCTCCAGCCCGGGGTCTCTGGAGCTG 1062
Db 490 GCTTGGGTGACACAGACCCCTGATCCCAATCCAGTCTTCAGAGCCTGGGGTCTCTGGAGCTG 549
QY 1063 CTTCTGGTTCAGTGGAGCAGCAGAGAGT 1093
Db 550 CTTCTGGTTCAGAGAACATGAAGAGAAAT 580

Search completed: November 8, 2004, 20:32:03
Job time : 8984.76 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 05:07:09 ; Search time 1316.86 Seconds
(without alignments)
7641.758 Million cell updates/sec

Title: US-09-937-636-2

Perfect score: 1917

Sequence: 1 atgctactgccaactgctgtct.....atgcagaagtcagtcca 1917

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134896 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_23Sep04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1917	100.0	1917	3	AAA37848 Human obe
2	1917	100.0	3099	2	AAV99912 Human sia
3	1917	100.0	3099	2	AAV99911 Human sia
4	1907.4	99.5	2295	3	AAA80610 Human CD3
5	1907.4	99.5	2295	9	ADA27034 Human nov
6	1907.4	99.5	2295	12	AD86564 Novel hum
7	1868	97.4	2954	6	ABK43361 DNA encod
8	1733	90.4	2208	6	ABK43367 DNA encod
9	1733	90.4	3024	6	ABK43373 DNA encod
10	1729.8	90.2	2176	12	ADI37009 Novel hum
11	1729.8	90.2	2176	12	ADL82804 Human PRO
12	1729.8	90.2	2338	9	ADA27152 Human nov
13	1721	89.8	3264	10	AD119239 Human CDN
14	1497.4	78.1	2823	6	ABK43362 DNA encod
15	1337	69.7	2565	6	ABK43360 DNA encod
16	1333.8	69.6	2764	2	Aaz34109 Human PRO
17	1333.8	69.6	2764	3	AAC78510 Human PRO
18	1333.8	69.6	2764	4	AAS45983 Human DNA
19	1333.8	69.6	2764	8	ACA63677 Novel hum
20	1333.8	69.6	2764	8	ACA9433 cDNA enco
21	1333.8	69.6	2764	8	ACA73443 Human sec

22	1333.8	69.6	2764	8	ACA05758 Human sec
23	1333.8	69.6	2764	8	ACA66592 CDNA enco
24	1333.8	69.6	2764	8	ACF20167 Human sec
25	1333.8	69.6	2764	8	ACF19553 Human sec
26	1333.8	69.6	2764	8	ACD21841 Human sec
27	1333.8	69.6	2764	8	ACD21841 Human sec
28	1333.8	69.6	2764	8	ACD21841 Human sec
29	1333.8	69.6	2764	8	ACD21841 Human sec
30	1333.8	69.6	2764	8	ACD21841 Human sec
31	1333.8	69.6	2764	8	ACD21841 Human sec
32	1333.8	69.6	2764	8	ACD21841 Human sec
33	1333.8	69.6	2764	8	ACD21841 Human sec
34	1333.8	69.6	2764	8	ACD21841 Human sec
35	1333.8	69.6	2764	8	ACD21841 Human sec
36	1333.8	69.6	2764	8	ACD21841 Human sec
37	1333.8	69.6	2764	8	ACD21841 Human sec
38	1333.8	69.6	2764	8	ACD21841 Human sec
39	1333.8	69.6	2764	8	ACD21841 Human sec
40	1333.8	69.6	2764	8	ACD21841 Human sec
41	1333.8	69.6	2764	8	ACD21841 Human sec
42	1333.8	69.6	2764	8	ACD21841 Human sec
43	1333.8	69.6	2764	8	ACD21841 Human sec
44	1333.8	69.6	2764	8	ACD21841 Human sec
45	1333.8	69.6	2764	8	ACD21841 Human sec

ALIGNMENTS

RESULT 1
AAA37848
ID AAA37848 standard; DNA; 1917 BP.
XX
AC AAA37848;
XX
DT 12-FEB-2001 (first entry)
XX
DE Human obesity protein binding protein-2 homologue coding sequence #2.
XX
KW Human obesity protein binding protein-2 homologue; hOB-BP2h; obesity;
XX
OS Homo sapiens.
XX
FH Key
FT CDS
FT Location/Qualifiers
FT 1..1917
FT /*tag= a
FT /product= "hOB-BP2h"
XX
PN WO200059942-A2.
XX
PD 12-OCT-2000.
XX
PF 22-MAR-2000; 2000WO-US006692.
XX
XX
XX 02-APR-1999; 99US-0127667P.
XX
XX (ELIL) LILLY & CO ELI.
XX
XX Su EW, Wei J;
XX WPI; 2000-664992/64.
XX P-PSDB; AAY97543.
XX
XX New human obesity protein binding protein-2 homologue nucleic acids,
XX polynucleotides and polypeptides useful for producing medicament for
XX treating obesity and/or obesity-related disorders.
XX
XX Claim 3; Page 86; 92pp; English.
XX
XX This sequence encodes a human obesity protein binding protein-2 homologue
XX (hOB-BP2h) of the invention. The hOB-BP2h nucleic acids and polypeptides
XX may be used for the manufacture of a medicament for the treatment of

181 TTCAAAGCAGTGAAGCAACCAAGGGTGTCTCTGTGGCCACAAACACACAGAGTCGA 240
Db
231 TTCAAAGCAGTGAAGCAACCAAGGGTGTCTCTGTGGCCACAAACACACAGAGTCGA 290
Qy
241 GAGTGGAAATGAGCAACCCGGGGCCGATTCACAGCTCACTGGGGATCCCGCCAAAGGGGAAC 300
Db
291 GAGTGGAAATGAGCAACCCGGGGCCGATTCACAGCTCACTGGGGATCCCGCCAAAGGGGAAC 350
Qy
301 TGCTCTGTGTATCAGACGCGCAGATGCGAGATGAGTCAAGTACATCTCTTCGGGTG 360
Db
351 TGCTCTGTGTATCAGACGCGCAGATGCGAGATGAGTCAAGTACATCTCTTCGGGTG 410
Qy
361 GAGAGGAAGACTATGTGAGATATAATTTTCATGAACGATGGGTCTTTCTAAAAGTAAACA 420
Db
411 GAGAGGAAGACTATGTGAGATATAATTTTCATGAACGATGGGTCTTTCTAAAAGTAAACA 470
Qy
421 GTGTCAAGTTCACGCGCCAGACCCCGAGACCAACAACCGACTACCTGCGCATGTGGAC 480
Db
471 GTGTCAAGTTCACGCGCCAGACCCCGAGACCAACAACCGACTACCTGCGCATGTGGAC 530
Qy
481 TTCTCCAGAAAGGTGTGAGCGCACAGAGACCGTCCGACTCGGTGTGGCTATGCCCC 540
Db
531 TTCTCCAGAAAGGTGTGAGCGCACAGAGACCGTCCGACTCGGTGTGGCTATGCCCC 590
Qy
541 AGAGACCTTGTATACAGATTTTACGCTGACACACGCGCCCTGGAGCCCGACGCCCCAG 600
Db
591 AGAGACCTTGTATACAGATTTTACGCTGACACACGCGCCCTGGAGCCCGACGCCCCAG 650
Qy
601 GGAATGTCCATACCTGGAAGCCCAAAAGGCGAGTTCCTGGGCTCTCTGTGCTGCT 660
Db
651 GGAATGTCCATACCTGGAAGCCCAAAAGGCGAGTTCCTGGGCTCTCTGTGCTGCT 710
Qy
661 GAGAGCAGCCCTCTGCACACTGAGCTGGGTCTCTGAGAACAGAGTCTCTCTCTGCTC 720
Db
711 GAGAGCAGCCCTCTGCACACTGAGCTGGGTCTCTGAGAACAGAGTCTCTCTCTGCTC 770
Qy
721 CATCTCTGGGGCTTAGACCCCTGGGGCTGGAGCTGCCGGGTGAAGGCTGGGATTCGA 780
Db
771 CATCTCTGGGGCTTAGACCCCTGGGGCTGGAGCTGCCGGGTGAAGGCTGGGATTCGA 830
Qy
781 GGGGGCTACACCTTCCAGCGGAGAACAGGCTTGGCTCCAGCAGCGAGCCCTGGACCTC 840
Db
831 GGGGGCTACACCTTCCAGCGGAGAACAGGCTTGGCTCCAGCAGCGAGCCCTGGACCTC 890
Qy
841 TCTGTGAGTATCTCTCAGAGAACCTGAGAGTATGATGTTTCCCAAGCAACACAGACAGTC 900
Db
891 TCTGTGAGTATCTCTCAGAGAACCTGAGAGTATGATGTTTCCCAAGCAACACAGACAGTC 950
Qy
901 CTGGAAGAACTTGGAGCGCAGCTCTCTCCAGTACTGGAGGGCCAAAGCTCTGCTCG 960
Db
951 CTGGAAGAACTTGGAGCGCAGCTCTCTCCAGTACTGGAGGGCCAAAGCTCTGCTCG 1010
Qy
961 GTCTGTGTACACACAGCAGCCCGCCAGCCAGGCTGAGCTGGACCCAGAGGGGACAGGTT 1020
Db
1011 GTCTGTGTACACACAGCAGCCCGCCAGCCAGGCTGAGCTGGACCCAGAGGGGACAGGTT 1070
Qy
1021 CTGAGCCCTCTCCAGCCCTCAGACCCCGGGTCTCTGAGAGTGTCTCTGGGTTCAAGTGGAG 1080
Db
1071 CTGAGCCCTCTCCAGCCCTCAGACCCCGGGTCTCTGAGAGTGTCTCTGGGTTCAAGTGGAG 1130
Qy
1081 CACGAAGGAGGTTTCACTGCACTGCGCAGCCCTGAGCTGGCTCCAGCAGCTCTCTCTC 1140
Db
1131 CACGAAGGAGGTTTCACTGCACTGCGCAGCCCTGAGCTGGCTCCAGCAGCTCTCTCTC 1190
Qy
1141 AGCTCTCTCGTGAATACTCCCGAAGCTGCTGGGCCCCCTCTCTCTCTGGAGGCTGAG 1200
Db
1191 AGCTCTCTCGTGAATACTCCCGAAGCTGCTGGGCCCCCTCTCTCTCTGGAGGCTGAG 1250
Qy
1201 GGTCTGCACTGCACTGCTCTCTCCAGCCAGCCCGCCCCCTCTCTCTCTGGCTGCTGCT 1260
Db
1251 GGTCTGCACTGCACTGCTCTCTCCAGCCAGCCCGCCCCCTCTCTCTCTGGCTGCTGCT 1310
Qy
1261 GGGAGGAGCTGTGTGAGGGGAACAGCAGCCAGGACTCTCTCTGAGGTTCAACCCCAAGCTCA 1320

1311 GGGGAGGAGCTGTCTGGAGGGGNAACAGCAGCCAGGACTCTCTCGAGGTCACCCCAGCTCA 1370
Qy
1321 GCCGGGCTCTGGGCGCAACAGCTCTCTGAGCTCTCATGAGGGCTCAGTCTCGGCTCAGG 1380
Db
1371 GCCGGGCTCTGGGCGCAACAGCTCTCTGAGCTCTCATGAGGGCTCAGTCTCGGCTCAGG 1430
Qy
1381 CTCCGCTGTGAGGGCTGGAACGTCATCGGCGCCAGAGTGGATCCATCTCTCAGCTGGCA 1440
Db
1431 CTCCGCTGTGAGGGCTGGAACGTCATCGGCGCCAGAGTGGATCCATCTCTCAGCTGGCA 1490
Qy
1441 GATAAGAGGAGCTCATCTCAACGGCATTTCTCAACGGAGCGTTTCTGGGAATCGGCATC 1500
Db
1491 GATAAGAGGAGCTCATCTCAACGGCATTTCTCAACGGAGCGTTTCTGGGAATCGGCATC 1550
Qy
1501 ACGGCTCTCTTTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
Db
1551 ACGGCTCTCTTTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1610
Qy
1561 ACTCAGACAGAAACCCCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
Db
1611 ACTCAGACAGAAACCCCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1670
Qy
1621 AATGTGTCCGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
Db
1671 AATGTGTCCGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1730
Qy
1681 AGTCTCTCGACCCCTCTTCCACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
Db
1731 AGTCTCTCGACCCCTCTTCCACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1790
Qy
1741 AAGCAGTATCATGTTCCCGAGTTTCCAGAACCCAAATCATCTCAAGCCCGCAGATTC 1800
Db
1791 AAGCAGTATCATGTTCCCGAGTTTCCAGAACCCAAATCATCTCAAGCCCGCAGATTC 1850
Qy
1801 CAGGAGAGCCAGAGAGGCTCCATTTATCCAGCTTCCAGGCTTCCAGGCTGCTGAGCC 1860
Db
1851 CAGGAGAGCCAGAGAGGCTCCATTTATCCAGCTTCCAGGCTTCCAGGCTGCTGAGCC 1910
Qy
1861 CTGAGGCGCGGATGCCCAAGCGCACCCAGCGGATTTGAGAGTCAAGTTCCAA 1917
Db
1911 CTGAGGCGCGGATGCCCAAGCGCACCCAGCGGATTTGAGAGTCAAGTTCCAA 1967

RESULT 4

AAA80610

ID AAA80610 standard; cDNA; 2295 BP.

XX

AC AAA80610;

XX

DT 21-NOV-2000 (first entry)

XX

DE Human CD33-like secreted protein gene #5.

XX

Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
anti-rheumatic; dermatological; antiproliferative; antiarteriosclerotic;
anticancer; vulnary; antiviral; antibacterial; antifungal;
immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;
multiple sclerosis; inflammatory disorder; inflammatory bowel disease;
Crohn's disease; nephritis; hyperproliferative disorder;
cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;
melanoma; lymphoma; wound healing; human; ss.

XX Homo sapiens.

OS

XX WC200029435-A1.

XX

XX 25-MAY-2000.

XX

XX 27-OCT-1999; 99WO-US025031.

XX

XX 28-OCT-1998; 98US-0105971P.

XX

XX

421 GTGCTCAGCTTACGCCAGACCCAGGACCAAAACACGACCTCAGCTGCGATGTGGAC 480
 478 GTGCTCAGCTTACGCCAGACCCAGGACCAAAACACGACCTCAGCTGCGATGTGGAC 537
 481 TTCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGTGGGCTATGCCCC 540
 538 TTCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGTGGGCTATGCCCC 597
 541 AGAGACCTTGTATCAGCATTTTACGTGACAAACGCGACCGCTGTGAGGCCCGAGCCCCAG 600
 598 AGAGACCTTGTATCAGCATTTTACGTGACAAACGCGACCGCTGTGAGGCCCGAGCCCCAG 657
 601 GGAATGTCCCATACCTCTGGAAGCCCAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGCT 660
 658 GGAATGTCCCATACCTCTGGAAGCCCAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGCT 717
 661 GACAGCAGGCCCTGTGCGACATCTGAGTGTGGTCTCTGAGAACAGATTCCTCTCTCTGTC 720
 718 GACAGCAGGCCCTGTGCGACATCTGAGTGTGGTCTCTGAGAACAGATTCCTCTCTCTGTC 777
 721 CATCCCTGGGGCCCTAGACCCCTGGGCTGAGCTGCCGGGTGAAGGCTGGGGATTCA 780
 778 CATCCCTGGGGCCCTAGACCCCTGGGCTGAGCTGCCGGGTGAAGGCTGGGGATTCA 837
 781 GGGCGCTACACCTGCGGAGCGGAGAACAGGCTTGGCTCCACAGCAGGAGCCCTGGACCTC 840
 838 GGGCGCTACACCTGCGGAGCGGAGAACAGGCTTGGCTCCACAGCAGGAGCCCTGGACCTC 897
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 898 TCTGTGAGTATCTCCAGAGAACCTGAGAGTGAATGTTTCCCAAGCAACAGGACAGTC 957
 901 CTGGAAGACCTTGGGAACGCGAGCTCTCTCCAGTACTGGAGGGCCAAAGCCTGTGCCCTG 960
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 1081 CAGAGGAGAGTTCACCTGCCAGCTCTGCGACCCCACTGGGCTCCAGCAGCAGTCTCTCTC 1140
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 1141 AGCTCTCCGTCAGTACTCCCGAGAGCTGCTGGGCGCTCTGCTCTCTGGAGGCTGAG 1200
 1198 AGCTCTCCGTCAGTACTCCCGAGAGCTGCTGGGCGCTCTGCTCTCTGGAGGCTGAG 1257
 1201 GGTCTGCACTGCACTGCTCTCTCCAGGCGAGCCCGGCGCTCTCTGCGCTGGTGGCTT 1260
 1258 GGTCTGCACTGCACTGCTCTCTCCAGGCGAGCCCGGCGCTCTCTGCGCTGGTGGCTT 1317
 1261 GGGGAGAGCTGTGAGGGGAAACAGCAGCAGGACTCTCTGAGGTCAACCCAGCTCA 1320
 1318 GGGGAGAGCTGTGAGGGGAAACAGCAGCAGGACTCTCTGAGGTCAACCCAGCTCA 1377
 1321 GCCGGGCGCTGGGCGCAACAGCTCCCTGAGCTCCATGGAGGGCTCAGCTCCGGGCTCAGG 1380
 1378 GCCGGGCGCTGGGCGCAACAGCTCCCTGAGCTCCATGGAGGGCTCAGCTCCGGGCTCAGG 1437
 1381 CTCGGTGTGAGGCTGTGAACAGTCCATGGGGCCCAAGTGGATCCATCTGTGAGTGGCA 1440
 1438 CTCGGTGTGAGGCTGTGAACAGTCCATGGGGCCCAAGTGGATCCATCTGTGAGTGGCA 1497
 1441 GATAAGAGGAGTCACTCAACGGGATTTCTCCACGGAGCGTTCTTGGGAATCGGCATC 1500
 1498 GATAAGAGGAGTCACTCAACGGGATTTCTCCACGGAGCGTTCTTGGGAATCGGCATC 1557

1501 ACGGCTCTCTTTTCTCTGCTGCTGCTGATCATCATGAAGATTCTACCGAAGAGCGG 1560
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 1621 AATGTGTCCCGACCGCTGGGCCCTCTGCTCAGAAAGCGGAATCAGAAAGCCACACCAAC 1680
 1678 AATGTGTCCCGACCGCTGGGCCCTCTGCTCAGAAAGCGGAATCAGAAAGCCACACCAAC 1737
 1681 AGTCTCTCGGACCCCTCTTCCACACGAGTCTCTCCCTCCCGAGAAATCAAGAAAGAACAGAAA 1740
 1738 AGTCTCTCGGACCCCTCTTCCACACGAGTCTCTCCCTCCCGAGAAATCAAGAAAGAACAGAAA 1797
 1741 AAGCAGTATCAGTTGCCCCAGTTTCCAGAACCCAAATCATCCACTCAAGCCCCAGAAATCC 1800
 1798 AAGCAGTATCAGTTGCCCCAGTTTCCAGAACCCAAATCATCCACTCAAGCCCCAGAAATCC 1857
 1801 CAGGAGAGCCAGAGGAGCTCCATTATGCCACGCTCACTTCCAGGGGTCCAGACCCAGG 1860
 1858 CAGGAGAGCCAGAGGAGCTCCATTATGCCACGCTCACTTCCAGGGGTCCAGACCCAGG 1917
 1861 CTTGAGGCCCGGATGCCCCAAGGGCACCCAGGCGGATTATGAGAAAGTCAAGTTCCAA 1917
 1918 CTTGAGGCCCGGATGCCCCAAGGGCACCCAGGCGGATTATGAGAAAGTCAAGTTCCAA 1974

RESULT 6

ADE86564

ID ADE86564 standard; cDNA; 2295 BP.

AC ADE86564;

XX AC ADE86564;

DT 29-JAN-2004 (first entry)

XX Novel human secreted protein cDNA #5.

DE human; ss; gene; secreted protein; cancer; liver disorder; hepatitis;
 KW neural disorder; Alzheimer's disease.
 XX Homo sapiens.

OS Homo sapiens.

XX US2003:129685-A1.

PN 10-JUL-2003.

XX 18-APR-2001; 2001US-00836353.

XX 28-OCT-1998; 98US-0105971P.

XX 27-OCT-1999; 99WO-US025031.

XX 19-APR-2000; 2000US-0198407P.

XX {NIJ/J} NI J.

PA {YOUNG} YOUNG P E.

PA {Kenny} KENNY J J.

PA {OLSEN} OLSEN H S.

PA {MOORE} MOORE P A.

PA {WEI} WEI Y.

PA {GREENE} GREENE J M.

PA {RUBEN} RUBEN S M.

XX Ni J, Young PE, Kenny JJ, Olsen HS, Moore PA, Wei Y, Greene JM;

PI Ruben SM;

XX WPI; 2004-020335/02.

XX P-PSDB; ADE86582.

XX New nucleic acid molecule, useful for preparing a medicament for

XX preventing, treating or ameliorating a medical condition e.g. cancer,

XX liver disorders or neural disorders.

	Claim 4; SEQ ID NO 15; 380pp; English.	
PS	The invention relates to an isolated nucleic acid sequence, or its	
XX	allelic variant, a fragment of the cDNA sequence, or its fragment,	
CC	domain, epitope or species homologue. The nucleic acid is useful for	
CC	preparing a medicament for preventing, treating or ameliorating a medical	
CC	condition e.g., cancer, liver disorders such as hepatitis or neural	
CC	disorders such as Alzheimer's disease. The present sequence represents	
CC	cDNA encoding a novel human secreted protein.	
XX		
SQ	Sequence 2295 BP; 494 A; 732 C; 620 G; 449 T; 0 U; 0 Other;	
	Query Match 99.5%; Score 1907.4; DB 12; Length 2295;	
	Best Local Similarity 99.7%; Pred. No. 0;	
	Matches 1911; Conservative 0; Mismatches 6; Indels 0; Gaps 0;	
QY	1 ATGCTACTGCCAAGTGTTCGGTGCGATGCACCAAGCATTGGAGTTGGATGGAGA 60	Dt
Tc	58 ATGCTACTGCCAAGTGTTCGGTGCGATGCACCAAGCATTGGAGTTGGATGGAGA 117	
QY	61 TTCTGGATACGAATCACGAATCATGATGTCGCGAGGCGCTGTCATCTCTGTGCC 120	
Tc	118 TTCTGGATACGAATCACGAATCATGATGTCGCGAGGCGCTGTCATCTCTGTGCC 177	
QY	121 TGCTCTTTCTCTACCCTCCGACAAGACATGCACAGGCTCTACCCCAGCTTAATGGCTACTGG 180	
Tc	178 TGCTCTTTCTCTACCCTCCGACAAGACATGCACAGGCTCTACCCCAGCTTAATGGCTACTGG 237	
QY	181 TTCAAAGCAGTAGTGCAGAACACCAAGGGTCTCTGTGGCCACAAAACCAAGAGTCGA 240	
Tc	238 TTCAAAGCAGTAGTGCAGAACACCAAGGGTCTCTGTGGCCACAAAACCAAGAGTCGA 297	
QY	241 GAGGTGGAATCAGCACCCGGGGCCGATTCAGAGTCTACCTGGGGATCCCGCAAAGGGGAAC 300	
Tc	298 GAGGTGGAATCAGCACCCGGGGCCGATTCAGAGTCTACCTGGGGATCCCGCAAAGGGGAAC 357	
QY	301 TGCTCTCTGGTGAATCAGAGACCGCGAGATGCAGAGTAGTGCAGATCTCTTTCCGGGTG 360	
Tc	358 TGCTCTCTGGTGAATCAGAGACCGCGAGATGCAGAGTAGTGCAGATCTCTTTCCGGGTG 417	
QY	361 GAGAGAGGAAGTATGTGAGATAATTTTCATGAACGATGGTTCTTTCTAAAAAGTAACA 420	
Tc	418 GAGAGAGGAAGTATGTGAGATAATTTTCATGAACGATGGTTCTTTCTAAAAAGTAACA 477	
QY	421 GTGCTCAGCTTTCAGCCCCAGACCCAGGACCAACACCCGACCTCACTGCCATGTGGAC 480	
Tc	478 GTGCTCAGCTTTCAGCCCCAGACCCAGGACCAACACCCGACCTCACTGCCATGTGGAC 537	
QY	481 TTTCTCAGAAAGGGTGTGACCGACAGAGGACCGTCCGACTCCGTGTGGCTATGCCCCC 540	
Tc	538 TTTCTCAGAAAGGGTGTGACCGACAGAGGACCGTCCGACTCCGTGTGGCTATGCCCCC 597	
QY	541 AGAGACCTTTGTATCAGCATTTTCAGTGCACAAACGCCAGGCCCTGGAGCCGCCAGCCCCAG 600	
Tc	598 AGAGACCTTTGTATCAGCATTTTCAGTGCACAAACGCCAGGCCCTGGAGCCGCCAGCCCCAG 657	
QY	601 GGAAATGTGCCATACCTGGAAGCCCAAAAGGCCAGTTCTTGGGGTCTCTGTGTGGTCT 660	
Tc	658 GGAAATGTGCCATACCTGGAAGCCCAAAAGGCCAGTTCTTGGGGTCTCTGTGTGGTCT 717	
QY	661 GACAGCAGCCCTGCCACACTGAGCTGGGTCCTGCAGAAACAGAGTCTCTCTCGTCC 720	
Tc	718 GACAGCAGCCCTGCCACACTGAGCTGGGTCCTGCAGAAACAGAGTCTCTCTCGTCC 777	
QY	721 CATCTCTGGGGCCCTTAGAAGCTTGGAGTGTGCCCGGGGTGAAGGCTGGGGGATCCA 780	
Tc	778 CATCTCTGGGGCCCTTAGAAGCTTGGAGTGTGCCCGGGGTGAAGGCTGGGGGATCCA 837	
QY	781 GGGCGGTACACCTGCGAGCGAGAACAGGCTTGGCTCCAGACGCGAGCCCTGCAGCTC 840	
Tc	838 GGGCGGTACACCTGCGAGCGAGAACAGGCTTGGCTCCAGACGCGAGCCCTGCAGCTC 897	
Qy	841 TCCTGTGAGTATCTCCAGAGAACCTTGAGTGATGTGGTTTTCCCAAGCAAAACAGACAGTC 900	
		RESULT 7

RESULT. 7

538 GGCCTGACTCAGAGCCTGATGTCTATCATCCCGAGACCCCTGGAGCCGGCGACGGGTG 597
419 ----- 418
598 ACGGTCTATCTGTGTGTTAACTGGGCTTTGAGGAATGTCCACCCCTTCTTCTCTCTGG 657
419 -----CAGTGCTC 426
658 ACGGGGTGTCCTCTCTCTCCCAAGGACCAACCAAGACCTCCCACTTCTCAGTGCTC 717
427 AGCTTCAGCCCGAGACCCCGAGACCAACACCGACCTCAGCTGCCATGTGAGACTTCTCC 486
718 AGCTTCAGCCCGAGACCCCGAGACCAACACCGACCTCAGCTGCCATGTGAGACTTCTCC 777
487 AGAAGGGTGTGAGCGCACAGAGACCGTCCGACTCTCCGTGTGGCTATGCCCCAGAGAC 546
778 AGAAGGGTGTGAGCGCACAGAGACCGTCCGACTCTCCGTGTGGCTATGCCCCAGAGAC 837
547 CTGTGTATCAGCATTTACGTGACAAACACCGACCTGGAGCCCGAGCCCGAGGAAAT 606
838 CTGTGTATCAGCATTTACGTGACAAACACCGACCTGGAGCCCGAGCCCGAGGAAAT 897
607 GTCCCATACCTGGAAGCCCAAAAGGCCAGTTCTCTGGGCTCTCTGTGTGTGTGACGC 666
898 GTCCCATACCTGGAAGCCCAAAAGGCCAGTTCTCTGGGCTCTCTGTGTGTGTGACGC 957
667 CAGCCCTCTGCCACACTGAGCTGGGTCTCTGAGAACAGAGTCTCTCTCTCTCTCTCTCTCC 726
958 CAGCCCTCTGCCACACTGAGCTGGGTCTCTGAGAACAGAGTCTCTCTCTCTCTCTCTCTCC 1017
727 TGGGGCCCTAGACCCCTGGGGCTGGAGTGCCTGGGCTGAGGCTGGGATTCAGGGCCG 786
1018 TGGGGCCCTAGACCCCTGGGGCTGGAGTGCCTGGGCTGAGGCTGGGATTCAGGGCCG 1077
787 TACACCTGCCAGCGGAGAACAGAGCTTTGGCTCCAGCAGCAGCCCTGGACCTCTCTGTG 846
1078 TACACCTGCCAGCGGAGAACAGAGCTTTGGCTCCAGCAGCAGCCCTGGACCTCTCTGTG 1137
847 CAGTATCTCCAGAGAACCTGAGAGTGAATGGTTTCCCAAGCAACAGACAGTCTCTGGAA 906
1138 CAGTATCTCCAGAGAACCTGAGAGTGAATGGTTTCCCAAGCAACAGACAGTCTCTGGAA 1197
907 AACCTTGGAGACGACGTCTCTCCAGTACTGGAGGCGCAAGGCTGTGCTGTGTGTGT 966
1198 AACCTTGGAGACGACGTCTCTCCAGTACTGGAGGCGCAAGGCTGTGCTGTGTGTGT 1257
967 GTCACACAGCAGCAGCCCGCAGCAGCTGAGCTGGACCCAGAGGGACAGGTTCTGAGC 1026
1258 GTCACACAGCAGCAGCCCGCAGCAGCTGAGCTGGACCCAGAGGGACAGGTTCTGAGC 1317
1027 CCCTCCAGCCCTCAGACCCCGGGTCTCTGAGCTGCTCGGTTCAAGTGGAGCAGGAA 1086
1318 CCCTCCAGCCCTCAGACCCCGGGTCTCTGAGCTGCTCGGTTCAAGTGGAGCAGGAA 1377
1087 GGAGAGTTACCTGCCACGCTCGGACCCCTCTGGGCTCCAGCAGCTCTCTCTCAGCCTC 1146
1378 GGAGAGTTACCTGCCACGCTCGGACCCCTCTGGGCTCCAGCAGCTCTCTCTCAGCCTC 1437
1147 TCCTGACACTCTCCGAGAGCTGTCTGGGCGCTCTCTGCTCTCTGAGAGCTGAGGCTCTG 1206
1438 TCCTGACACTCTCCGAGAGCTGTCTGGGCGCTCTCTGCTCTCTGAGAGCTGAGGCTCTG 1497
1207 CACTGACAGTGTCTCTCCAGGCGCAGCCCGCCCTCTCTGCTGTGGTGTGGGGAG 1266
1498 CACTGACAGTGTCTCTCCAGGCGCAGCCCGCCCTCTCTGCTGTGGTGTGGGGAG 1557
1267 GAGCTGTGGAGGGGAAACAGCAGCCAGGACTCTCTTGGAGTCAACCCCTCAGCTCAGCCGG 1326
1558 GAGCTGTGGAGGGGAAACAGCAGCCAGGACTCTCTTGGAGTCAACCCCTCAGCTCAGCCGG 1617
1327 CCCTGGGCCAACAGCTCTCTGAGCTCTCCATGGAGGGCTCAGGCTCGGCTCAGGCTCCGC 1386
1618 CCCTGGGCCAACAGCTCTCTGAGCTCTCCATGGAGGGCTCAGGCTCGGCTCAGGCTCCGC 1677

1387 TGTGAGGCTGGAACGTCCATGGGGCCAGAGTGGATCCATCTCGAGCTGCCAGATAAG 1446
1678 TGTGAGGCTGGAACGTCCATGGGGCCAGAGTGGATCCATCTCGAGCTGCCAGATAAG 1737
1447 AAGGAGACTCATCTCAACGGCAATTTCCCAACGGAGCGTTTCTGGGAATCGGCATCAGGCT 1506
1738 AAGGAGACTCATCTCAACGGCAATTTCCCAACGGAGCGTTTCTGGGAATCGGCATCAGGCT 1797
1507 CTCTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1566
1798 CTCTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1857
1567 ACAGAAACCCCGAGGCGCCAGGTTCTCCCGGCAACAGCAGGATCTCTGATTAATCAATGTG 1626
1858 ACAGAAACCCCGAGGCGCCAGGTTCTCCCGGCAACAGCAGGATCTCTGATTAATCAATGTG 1917
1627 GTCCCGAGCGCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1686
1918 GTCCCGAGCGCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1977
1687 CGGACCCCTCTCTCCACCGAGTCTCTCCCTCCAGAAATCAAGAAAGCAACAGAAAGCAG 1746
1978 CGGACCCCTCTCTCCACCGAGTCTCTCCCTCCAGAAATCAAGAAAGCAACAGAAAGCAG 2037
1747 TATCAGTTGCCAGTTTCCAGAAACCCAAATCAATCCACTCAAGGCCCAAGATCCCAAGAG 1806
2038 TATCAGTTGCCAGTTTCCAGAAACCCAAATCAATCCACTCAAGGCCCAAGATCCCAAGAG 2097
1807 AGCCAGAGGAGCTCCATTTATGCGAGCTCAACTTCCAGGGCTCAGACCCAGGCTCAG 1866
2098 AGCCAGAGGAGCTCCATTTATGCGAGCTCAACTTCCAGGGCTCAGACCCAGGCTCAG 2157
1867 GCGCGGATGCCCAAGGCGCACCCAGCGGATTTATGAGAAAGTCAAGTTTCCAA 1917
2158 GCGCGGATGCCCAAGGCGCACCCAGCGGATTTATGAGAAAGTCAAGTTTCCAA 2208

RESULT 9

ABK43373

ID ABK43373 standard; cDNA; 3024 BP.

XX AC ABK43373;

XX DT 05-JUN-2002 (first entry)

XX DE DNA encoding sialic acid-binding Ig-related lectin, Siglec-BMS-L3-995-2.

XX KW Human; sialic acid-binding Ig-related lectin; SIGLEC; asthma;
immune system disease; leukaemia; allergy; inflammatory disease;
tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease;
psoriasis; rheumatoid arthritis; conjunctivitis; gene; ss.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200208257-A2.

XX PD 31-JAN-2002.

XX PF 20-JUL-2001; 2001WO-US023082.

XX PR 21-JUL-2000; 2000US-0220139P.

XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX PI Longphre M, Chang H, Whitney G;

XX DR WPI; 2002-241565/29.

XX DR P-PSDB; AAU87087.

XX PT Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein
molecules useful for treating immune system diseases such as asthma,

Db 758 CTTGTTATCAGCAATTCACGTGACACACGCCAGCCCTCGAGGCCCCAGCCCGAGGAAT 817
Qy 607 GTCCCATACCTGGAAGCCCAAAAGCCAGTTCCTCGGCTCCTCTGCTCTGACAGC 666
Db 818 GTCCCATACCTGGAAGCCCAAAAGCCAGTTCCTCGGCTCCTCTGCTCTGACAGC 877
Qy 667 CAGCCCTCCACACTGAGCTGGGTCCTGCAGAACAGAGTCTCTCCCTCGTCCCATCC 726
Db 878 CAGCCCTCCACACTGAGCTGGGTCCTGCAGAACAGAGTCTCTCTCTGCTCCCATCC 937
Qy 727 TGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGTGAAGGCTGGGGATTCAGGGGC 786
Db 938 TGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGTGAAGGCTGGGGATTCAGGGGC 997
Qy 787 TACACCTCCGAGGAGAACAGCTTGGCTCCACAGGAGGCCCTGAGACTCTCTG 846
Db 998 TACACCTCCGAGGAGAACAGCTTGGCTCCACAGGAGGCCCTGAGACTCTCTG 1057
Qy 847 CAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAAAGGACAGCTCTGGAA 906
Db 1058 CAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAAAGGACAGCTCTGGAA 1117
Qy 907 AACCTTGGGAACGGGACGCTCTCCAGTACTGGAGGGCCAAAGCCTGTGCTGTCTGT 966
Db 1118 AACCTTGGGAACGGGACGCTCTCCAGTACTGGAGGGCCAAAGCCTGTGCTGTCTGT 1177
Qy 967 GTCACACACAGCAGCCCCCAGCAGCGCTGAGCTGGACCCAGAGGGGACAGGTTCTGAGC 1026
Db 1178 GTCACACACAGCAGCCCCCAGCAGCGCTGAGCTGGACCCAGAGGGGACAGGTTCTGAGC 1237
Qy 1027 CCTCTCCAGCCCTCAGACCCCGGGTCTGAGCTGCTGGGTTCAAGTGAGACAGAA 1086
Db 1238 CCTCTCCAGCCCTCAGACCCCGGGTCTGAGCTGCTGGGTTCAAGTGAGACAGAA 1297
Qy 1087 GGAGAGTTACCTGCCACGCTCGGACCCACTGGGCTCCAGCAGCTCTCTCAGCTC 1146
Db 1298 GGAGAGTTACCTGCCACGCTCGGACCCACTGGGCTCCAGCAGCTCTCTCAGCTC 1357
Qy 1147 TCCGTGCACTACTCCCGAAGCTGTGGGCCCCCTCTGCTCTCTGGAGGCTGAGGCTG 1206
Db 1358 TCCGTGCACTACTCCCGAAGCTGTGGGCCCCCTCTGCTCTCTGGAGGCTGAGGCTG 1417
Qy 1207 CACTGAGCTGCTCTCCAGGCGCAGCCCGCCCCCTCTCTGCGCTGGTGGTGGGAG 1266
Db 1418 CACTGAGCTGCTCTCCAGGCGCAGCCCGCCCCCTCTCTGCGCTGGTGGTGGGAG 1477
Qy 1267 GAGCTGCTGAGGGGAACAGCAGCAGGACTCTTCGAGGTACCCCCAGCTCAGCCGG 1326
Db 1478 GAGCTGCTGAGGGGAACAGCAGCAGGACTCTTCGAGGTACCCCCAGCTCAGCCGG 1537
Qy 1327 CCTGGGCCAACAGCTCCCTGAGCTCCATGAGGGCTGAGCTCCGGCTCAGGCTCCGC 1386
Db 1538 CCTGGGCCAACAGCTCCCTGAGCTCCATGAGGGCTGAGCTCTGGCTCAGGCTCCGC 1597
Qy 1387 TGTGAGCCTGGAAGCTCCATGGGCCCCAGAGTGGATCCATCTCGAGCTGCCAGATAAG 1446
Db 1598 TGTGAGCCTGGAAGCTCCATGGGCCCCAGAGTGGATCCATCTCGAGCTGCCAGATAAG 1657
Qy 1447 AAGGAGCTCATCTCAACGGGATTTCTCAACAGGAGCGCTTTCTGGGAATCGGCAATCAGGCT 1506
Db 1658 AAGGAGCTCATCTCAACGGGATTTCTCAACGGAGCGCTTTCTGGGAATCGGCAATCAGGCT 1717
Qy 1507 CTCTCTTCTCTGCTGGCCCTGATCATCATGAGATTCTACGAGAGAGAGAGGAGCTCAG 1566
Db 1718 CTCTCTTCTCTGCTGGCCCTGATCATCATGAGATTCTACCGAAGAGAGAGGAGCTCAG 1777
Qy 1567 ACAGAAACCCCGAGGCGCAGGTTCTCCCGGCACAGCAGGATCTCTGGATTACATCAATG 1626
Db 1778 ACAGAAACCCCGAGGCGCAGGTTCTCCCGGCACAGCAGGATCTCTGGATTACATCAATG 1837
Qy 1627 GTCCCGAGGCTGGCCCTCTGGCTCAGAGCGGAATCAGAAAGCCACACCAACAGTCTCT 1686
Db 1838 GTCCCGAGGCTGGCCCTCTGGCTCAGAGCGGAATCAGAAAGCCACACCAACAGTCTCT 1897

Qy 1687 CGGACCCCTCTTCCACAGGCTGCTCCCTCCCGAATCAAGAAAGACCAAGAGAGAG 1746
Db 1898 CGGACCCCTCTTCCACAGGCTGCTCCCTCCCGAATCAAGAAAGACCAAGAAAGAG 1957
Qy 1747 TATCAGTTGCCAGTTTCCAGAAACCCAAATCATCTCAAGCCCGCCAGATCCAGGAG 1806
Db 1958 TATCAGTTGCCAGTTTCCAGAAACCCAAATCATCTCAAGCCCGCCAGATCCAGGAG 2017
Qy 1807 AGCAAGAGGAGCTCCATTTATGCGACGCTCAACTTCCAGGCTCAGACCCAGGCTGAG 1866
Db 2018 AGCAAGAGGAGCTCCATTTATGCGACGCTCAACTTCCAGGCTCAGACCCAGGCTGAG 2077
Qy 1867 GCCCGGATGCCCAAGGGCAGCCAGCGGATTTATGCAAGTCAAGTTCCAA 1917
Db 2078 GCCCGGATGCCCAAGGGCAGCCAGCGGATTTATGCAAGTCAAGTTCCAA 2128

RESULT 11

ADL82804
ID ADL82804 standard; cDNA, 2176 BP.
XX AC ADL82804;
XX DT 17-JUN-2004 (first entry)
XX Human PRO71236 cDNA, SEQ ID 6.
XX Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
XX Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;
XX Gene Therapy; PRO; B cell related disorder; cancer;
XX immune-mediated inflammatory disease; human; gene; ss.
OS Homo sapiens.
XX WO2004024097-A2.
XX PD 25-MAR-2004.
XX PF 15-SEP-2003; 2003WO-US029097.
XX PR 16-SEP-2002; 2002US-0411392P.
XX (GETH) GENENTECH INC.
XX Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;
PI Wu TD;
XX WPI: 2004-329389/30.
XX P-PSDB; ADL82805.
XX New PRO polypeptide, useful for diagnosing and treating a B cell related
disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
XX Claim 2; Fig 6; 695pp; English.
XX The present invention relates to PRO proteins and their coding sequences.
The PRO proteins are useful for diagnosing and treating a B cell related
disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide
antigen unresponsiveness, selective IgA deficiency, selective IgM
deficiency, selective deficiency of IgG subclasses, immunodeficiency with
hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's
lymphoma, intermediate lymphoma, follicular lymphoma, type II
hyperimmunoreactivity, rheumatoid arthritis, autoimmune mediated hemolytic
anemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
ankylosing spondylitis. The PRO proteins are also useful for preparing a
medicament for treating a condition that is responsive to the PRO
protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
coding sequences are useful as hybridization probes in chromosome and
gene mapping, in preparing PRO proteins, or in generating transgenic
animals or knockout animals, which in turn are useful in the development
and screening of therapeutically useful reagents.

CC of the protein), preventing, treating or ameliorating a medical condition
CC by administering the nucleic acid or protein to a mammalian subject,
CC identifying a binding partner to the protein, the gene corresponding to
CC the cDNA sequence, and identifying an activity in a biological assay
CC (comprising expressing the nucleic acid in a cell, isolating the
CC supernatant, detecting an activity in a biological assay and identifying
CC the protein in the supernatant having the activity). The nucleic acids
CC and proteins display the following activities: Cytostatic, antibacterial,
CC Virocide, Neuroprotective, Gynaecological, Gastrointestinal-Gen,
CC Cardiant, Cardiovascular-Gen, Nephrotropic, Antiinflammatory, Muscular-
CC Gen, Respiratory-Gen, Immunosuppressive, Cerebroprotective, Vasotropic,
CC Nootropic, Antiallergic. The methods and compositions of the present
CC invention are useful for diagnosing, treating, preventing and/or
CC prognosticating disorders related to the novel polypeptides, such as
CC cancer, bacterial or viral infections, and neural, immune system, blood,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal, inflammatory or proliferative disorders (many examples of these
CC diseases and disorders are given in the specification). The present
CC sequence encodes a novel secreted protein of the invention.
XX
SQ Sequence 3264 BP; 804 A; 965 C; 849 G; 646 T; 0 U; 0 Other;

Query Match 89.8%; Score 1721; DB 10; Length 3264;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 1916; Conservative 0; Mismatches 0; Indels 175; Gaps 2;

QY 1 ATGCTACTGCACTGCTGCTCCTCGCTGCTGGCGGGTCCAGAGCTATGATGGAGA 60
DB 43 ATGCTACTGCACTGCTGCTCCTCGCTGCTGGCGGGTCCAGAGCTATGATGGAGA 102

QY 61 TTCTGGATACAGTGCAGGAGTCAGTATGATGTCGCGAGGGCTGTGCACTCTGTGCCC 120
DB 103 TTCTGGATACAGTGCAGGAGTCAGTATGATGTCGCGGA-GGCTGTGCACTCTGTGCCC 161

QY 121 TGCTCTTTCTCCTACCCGACAGACTGACAGAGGTCTACCCAGGCTTATGGCTACTGG 180
DB 162 TGCTCTTTCTCCTACCCGACAGACTGACAGAGGTCTACCCAGGCTTATGGCTACTGG 221

QY 181 TTCAAAGCAGTGTAGAGCAACCAAGGGTGTCTGTGGCCACAAACACACAGAGTCGA 240
DB 222 TTCAAAGCAGTGTAGAGCAACCAAGGGTGTCTGTGGCCACAAACACACAGAGTCGA 281

QY 241 GAGGTGAATATGACACCCGGGGCCGATTCACGCTCACTGGGATCCCGCAAGGGGAAC 300
DB 282 GAGGTGAATATGACACCCGGGGCCGATTCACGCTCACTGGGATCCCGCAAGGGGAAC 341

QY 301 TGCTCTTTGTGTATCAGACGCGCAGATGACAGATGAGTCAGTACTTTCTTGGGTG 360
DB 342 TGCTCTTTGTGTATCAGACGCGCAGATGACAGATGAGTCAGTACTTTCTTGGGTG 401

QY 361 GAGAGGAAAGCTATGTAGATATAATTTTCATGAACGATGGGTCTTTCTTAAAGTAA-- 418
DB 402 GAGAGGAAAGCTATGTAGATATAATTTTCATGAACGATGGGTCTTTCTTAAAGTAA 461

QY 419 ----- 418
DB 462 GCCTGTACTCAGAAGCCTGATGTCTACATCCCGAGACCTGTGAGCCCGGGGACGCCGTG 521

QY 419 ----- 418
DB 522 ACGETCATCTGTGTGTTTAACTGGGCTTTGAGGAATGTCCACCCCTTTCTCTCTGG 591

QY 419 -----CAGTGCTC 426
DB 582 ACGGGGCTGCCCTCTCCTCCCAAGGAACCAACACGACCTCCCACTTCTCAGTGCTC 641

QY 427 AGCTTTCACGGCCAGACCCCGAGGACCAACACCGACCTCACCTGCGCATGTGGATCTCTCC 486
DB 642 AGCTTTCACGGCCAGACCCCGAGGACCAACACCGACCTCACCTGCGCATGTGGATCTCTCC 701

QY 487 AGAAAGGGTGTGACGCGACAGAGAACCGTCCGACTCCGCTGTGGGCTATGCCGCCAGAGAC 546
DB 702 AGAAAGGGTGTGACGCGACAGAGAACCGTCCGACTCCGCTGTGGGCTATGCCGCCAGAGAC 761

QY 547 CTTGTTATCAGCATTTACGTGACAAACACGCGCAGCCCTGGAGCCCGCCAGGGAAT 606
DB 762 CTTGTTATCAGCATTTACGTGACAAACACGCGCAGCCCTGGAGCCCGCCAGGGAAT 821

QY 607 GTCCCATACCTTGAAGCCCAAAAAGGCCAGTCTCTGGGGCTCCTCTGTGCTGTGACAGC 666
DB 822 GTCCCATACCTTGAAGCCCAAAAAGGCCAGTCTCTGGGGCTCCTCTGTGCTGTGACAGC 881

QY 667 CAGCCCTCTGACACACTAGGTGGTCTTGAGAACAGAGTCTCTCTCTCTCTCTCTCTCT 726
DB 882 CAGCCCTCTGACACACTAGGTGGTCTTGAGAACAGAGTCTCTCTCTCTCTCTCTCTCT 941

QY 727 TGGGGCCCTAGACCCCTGGGCTCGAGTGCCTGGGGTGAAGGCTGGGGATTCAGGGGCG 786
DB 942 TGGGGCCCTAGACCCCTGGGCTCGAGTGCCTGGGGTGAAGGCTGGGGATTCAGGGGCG 1001

QY 787 TACACCTCCAGCGGAGAAACAGGCTTGGCTCCAGCAGCAGCCCTTGAGACTCTCTGTG 846
DB 1002 TACACCTCCAGCGGAGAAACAGGCTTGGCTCCAGCAGCAGCCCTTGAGACTCTCTGTG 1061

QY 847 CAGTATCTCCAGAGAACCTGAGTGTGATGATGATGATGATGATGATGATGATGATG 906
DB 1062 CAGTATCTCCAGAGAACCTGAGTGTGATGATGATGATGATGATGATGATGATGATG 1121

QY 907 AACCTTGGGAAACGGCACGCTCTCTCCAGTACTGGAGGGCCAAAGCCTGTGCTGTGT 966
DB 1122 AACCTTGGGAAACGGCACGCTCTCTCCAGTACTGGAGGGCCAAAGCCTGTGCTGTGT 1181

QY 967 GTACACACAGAGAGCCCTCCAGCAGGCTGAGCTGAGACCCAGAGGGGACAGGTTCTGAGC 1026
DB 1182 GTACACACAGAGAGCCCTCCAGCAGGCTGAGCTGAGACCCAGAGGGGACAGGTTCTGAGC 1241

QY 1027 CCTCTCCAGCCCTCAGACCCCGGGTCTCGAGTGTCTCGGGTCAAGTGGAGCAGCA 1086
DB 1242 CCTCTCCAGCCCTCAGACCCCGGGTCTCGAGTGTCTCGGGTCAAGTGGAGCAGCA 1301

QY 1087 GGAGATTTCACTGCTCCAGCTGGGACCCACTGGGGTCCAGAGAGTCTCTCTCAGCCTC 1146
DB 1302 GGAGATTTCACTGCTCCAGCTGGGACCCACTGGGGTCCAGAGAGTCTCTCTCAGCCTC 1361

QY 1147 TCCGTGCACTACTCCCGAAGCTGTGGGCCCTCTCTCTCTCTGGAGGCTGAGGCTCTG 1206
DB 1362 TCCGTGCACTACTCCCGAAGCTGTGGGCCCTCTCTCTCTCTGGAGGCTGAGGCTCTG 1421

QY 1207 CACTCAGCTGTCTCTCCAGCCAGCCCGGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1266
DB 1422 CACTCAGCTGTCTCTCCAGCCAGCCCGGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1481

QY 1267 GAGCTGTGGAGGGAAACAGACCCAGGACTCTCTCGAGGTCAACCCAGCTCAGCCGG 1326
DB 1482 GAGCTGTGGAGGGAAACAGACCCAGGACTCTCTCGAGGTCAACCCAGCTCAGCCGG 1541

QY 1327 CCTGGGCAACAGCTCCTCAGCCTCCATGGAGGGCTCAGCTCCGGCTCAGGCTCCGC 1386
DB 1542 CCTGGGCAACAGCTCCTCAGCCTCCATGGAGGGCTCAGCTCCGGCTCAGGCTCCGC 1601

QY 1387 TGTAGGGCTGGAACGCTCCATGGGGCCAGAGTGGATCCATCTCTCAGCTGCCAGATAG 1446
DB 1602 TGTAGGGCTGGAACGCTCCATGGGGCCAGAGTGGATCCATCTCTCAGCTGCCAGATAG 1661

QY 1447 RAGGCACTCATCTCAACGGCAATTTCTCAACGGAGGGTCTTCTGGGAATCGGCATCACGGCT 1506
DB 1662 RAGGCACTCATCTCAACGGCAATTTCTCAACGGAGGGTCTTCTGGGAATCGGCATCACGGCT 1721

QY 1507 CTTCTTTTCTCTGCTGGCCCTGATCATATGAAGATTTCTACCGAAGAGCGGACTCAG 1566
DB 1722 CTTCTTTTCTCTGCTGGCCCTGATCATATGAAGATTTCTACCGAAGAGCGGACTCAG 1781

QY 1567 ACAGAAACCCCGAGCCCGAGGTTCTCCGGGACAGCAGATCTCTGATTTACATCAATGTG 1626
DB 1782 ACAGAAACCCCGAGCCCGAGGTTCTCCGGGACAGCAGATCTCTGATTTACATCAATGTG 1841

1627 GTCCGACGGCTGCCCCCTGGCTCAGAGCGGAATCAGAAAGCCACCAACAGTCCT 1686
 1842 GTCCGACGGCTGCCCCCTGGCTCAGAGCGGAATCAGAAAGCCACCAACAGTCCT 1901
 1687 CGGACCCCTCTTCCACCAAGGTGCTCCCTCCCAAGATCAAGAGGAGAACCAAGAGCAG 1746
 1902 CGGACCCCTCTTCCACCAAGGTGCTCCCTCCCAAGATCAAGAGGAGAACCAAGAGCAG 1961
 1747 TATCAGTTGCCAGTTCCCGAGAACCAAGATCAAGATCAAGATCAAGATCAAGATCAAGAT 1806
 1962 TATCAGTTGCCAGTTCCCGAGAACCAAGATCAAGATCAAGATCAAGATCAAGATCAAGAT 2021
 1807 AGCCAAGAGGAGCTCCATTATGCAACGCTCAACTTCCCGAGGCGTCAGACCCAGGCTGAG 1866
 2022 AGCCAAGAGGAGCTCCATTATGCAACGCTCAACTTCCCGAGGCGTCAGACCCAGGCTGAG 2081
 1867 GCCCGGATGCCCAAGGCGACCCAGGCGGATTCAGAGATCAAGTTCCAA 1917
 2082 GCCCGGATGCCCAAGGCGACCCAGGCGGATTCAGAGATCAAGTTCCAA 2132

RESULT 14

ABK43362
 ID ABK43362 standard; cDNA; 2823 BP.

XX
 AC ABK43362;

XX
 DT 05-JUN-2002 (first entry)

XX
 DE DNA encoding sialic acid-binding Ig-related lectin, Siglec-BMS-L3c.

XX
 KW Human; sialic acid-binding Ig-related lectin; SIGLEC; asthma;
 immune system disease; leukaemia; allergy; inflammatory disease;
 tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease;
 psoriasis; rheumatoid arthritis; conjunctivitis; gene; ss.

XX
 OS Homo sapiens.

XX
 PN WO200208257-A2.

XX
 JB 31-JAN-2002.

XX
 EF 20-JUL-2001; 2001WO-US023082.

XX
 FR 21-JUL-2000; 2000US-0220139P.

XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX
 PI Longphre M, Chang H, Whitney G;

XX
 DR WPI; 2002-241565/29.

XX
 P-PSDB; AAU87076.

PT Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein
 molecules useful for treating immune system diseases such as asthma,
 leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease.

XX
 PS Claim 11; Fig 4A; 209pp; English.

XX
 CC The invention relates to an isolated SIGLEC (sialic acid-binding Ig-
 related lectin) protein (I). Pharmaceutical compositions comprising (I)
 are useful for treating immune system diseases such as asthma, leukaemia
 or other allergic or inflammatory diseases. Extracellular domains of (I)
 represent potential markers for screening, diagnosis, prognosis, follow-
 up assays, and imaging methods. (I) is useful as a target for drugs which
 inhibit inflammation, tissue damage and remodeling in asthma, and
 inflammatory diseases such as allergic rhinitis, osteoarthritis, Crohn's
 disease, psoriasis, rheumatoid arthritis, conjunctivitis, etc. (I) is
 also useful for monitoring the course of disease or disorders, and for
 identifying agents that bind with and/or modulate the biological activity
 of SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are
 useful in diagnosis and/or prognosis methods, and to detect the presence
 and/or amount of SIGLEC-BMS nucleotide sequences and/or SIGLEC-BMS

CC proteins in a biological sample. (II) are useful as nucleic acid probes
 are useful for screening genomic library to isolate a genomic clone of
 SIGLEC gene. SIGLEC-BMS gene copy number is determined for detecting
 diseases or disorders associated with SIGLEC-BMS transcripts or proteins.
 CC The SIGLEC-BMS antibodies are also used to detect, sort or isolate cells
 expressing SIGLEC-BMS proteins and in diagnostic imaging technology.
 CC ABK43360-ABK43411 represent human SIGLEC coding sequences and PCR primers
 of the invention

XX
 SQ Sequence 2823 BP; 677 A; 855 C; 725 G; 566 T; 0 U; 0 Other;

Query Match 78.1%; Score 1497.4; DB 6; Length 2823;

Best Local Similarity 99.9%; Pred No. 0;

Matches 1498; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	419	CAGTCTCAGCTTCACGCCAGACCCAGAGACCAACACCGACCTACCTGCATGTGG	478
DB	238	CAGTCTCAGCTTCACGCCAGACCCAGAGACCAACACCGACCTACCTGCATGTGG	297
QY	479	ACTTCTCCAGAAAGGTGTGAGCGCACAGAGACCGTCCGACTCGTGTGCGCTATGCC	538
DB	298	ACTTCTCCAGAAAGGTGTGAGCGCACAGAGACCGTCCGACTCGTGTGCGCTATGCC	357
QY	539	CCAGAGACCTTGTATTACAGCATTTTACCGTGACACACCGCCAGCCCTGGAGCCGCC	598
DB	358	CCAGAGACCTTGTATTACAGCATTTTACCGTGACACACCGCCAGCCCTGGAGCCGCC	417
QY	599	AGGGAATGTCCCATACCTGGAAGCCCAAAAGGCCAGTTCTCGGCTCTCTGTGCTG	658
DB	418	AGGGAATGTCCCATACCTGGAAGCCCAAAAGGCCAGTTCTCGGCTCTCTGTGCTG	477
QY	659	CTGACAGCAGCCGCCCTGCCACACTGAGCTGGGTCTCTGCAGAACAGAGTCTCTCTCGT	718
DB	478	CTGACAGCAGCCGCCCTGCCACACTGAGCTGGGTCTCTGCAGAACAGAGTCTCTCTCGT	537
QY	719	CCCATCTCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGCTGGGATT	778
DB	538	CCCATCTCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGCTGGGATT	597
QY	779	CAGGCGCTCAACCTCCGAGCGGAGAACAGGCTTGGCTCCACAGCAGGACCCCTGGACC	838
DB	598	CAGGCGCTCAACCTCCGAGCGGAGAACAGGCTTGGCTCCACAGCAGGACCCCTGGACC	657
QY	839	TCTCTGTGCATATCTCCAGAGAACTTGAGATGATGTTTCCCAAGCAAAAGAGCAG	898
DB	658	TCTCTGTGCATATCTCCAGAGAACTTGAGATGATGTTTCCCAAGCAAAAGAGCAG	717
QY	899	TCCTGGAAACCTTGGGAAACGCGACGCTCTCCAGTACTGGAGGGCCAAAGCCTGTGCC	958
DB	718	TCCTGGAAACCTTGGGAAACGCGACGCTCTCCAGTACTGGAGGGCCAAAGCCTGTGCC	777
QY	959	TGGTCTGTGCATACACAGCAGCCGCCAGCAGGCTGAGCTGGACCCAGAGGGGACAGG	1018
DB	778	TGGTCTGTGCATACACAGCAGCCGCCAGCAGGCTGAGCTGGACCCAGAGGGGACAGG	837
QY	1019	TCTGAGCCCTCTCCAGCCCTCAGACCCCGGGTCTCTGGAGCTGCCTCGGTTCAAGTGG	1078
DB	838	TCTGAGCCCTCTCCAGCCCTCAGACCCCGGGTCTCTGGAGCTGCCTCGGTTCAAGTGG	897
QY	1079	AGCAGAGGAGAGTTTACCTCTCCGACCGCTCCGACCCACCACTGGGCTCCAGCAGCTCTC	1138
DB	898	AGCAGAGGAGAGTTTACCTCTCCGACCGCTCCGACCCACCACTGGGCTCCAGCAGCTCTC	957
QY	1139	TCAGCTCTCCGTGCACTACTCTCCGAGAGTGTCTGGGCCCTCTCTGCTCTCTGGAGGCTG	1198
DB	958	TCAGCTCTCCGTGCACTACTCTCCGAGAGTGTCTGGGCCCTCTCTGCTCTCTGGAGGCTG	1017
QY	1199	AGGCTCTGCACTGAGCTGTCTCTCCAGGCGACCGCGGCCCTCTCTGCTCTGGTGGG	1258
DB	1018	AGGCTCTGCACTGAGCTGTCTCTCCAGGCGACCGCGGCCCTCTCTGCTCTGGTGGG	1077
QY	1259	TTGGGAGGAGAGTCTCTGGAGGGGAAACAGCAGCAGGACTCTCTGAGGTCAACCCAGCT	1318

541 AGAGACCTTGTATTACGATTTCACGTGACAAACAGCCAGCCCTGGAGCCCCCAGCCCCAG 600
1523
669 AGAGACCTTGTATTACGATTTCACGTGACAAACAGCCAGCCCTGGAGCCCCCAGCCCCAG 728
1740
601 GGAATGTCCTCATCTGGAGCCCAAAAGGCGAGTTCTCGGCTCTCTGTGTGCT 660
1583
729 GGAATGTCCTCATCTGGAGCCCAAAAGGCGAGTTCTCGGCTCTCTGTGTGCT 788
1800
661 GACAGCCAGCCCTGCGCACACTGAGCTGGTCTCTGAGAACAGATCTCTCTGTGTC 720
1643
789 GACAGCCAGCCCTGCGCACACTGAGCTGGTCTCTGAGAACAGATCTCTCTGTGTC 848
1860
721 CATCGCTGGGCTCTAGACCTCTGGGCTGGAGCTGGCCGGGTGAAGGCTGGGATTCA 780
1703
849 CATCGCTGGGCTCTAGACCTCTGGGCTGGAGCTGGCCGGGTGAAGGCTGGGATTCA 908
1917
781 GGGGCTACACCTCGAGCGGAGAACAGGCTTGGCTCCAGCAGCGAGCCCTGGACCTC 840
1760
909 GGGGCTACACCTCGAGCGGAGAACAGGCTTGGCTCCAGCAGCGAGCCCTGGACCTC 968
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841 TCTGTGAGTATCTCCAGAGAACTCAGAGTATGATGTTTCCAGCAAAACAGACATC 900
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969 TCTGTGAGTATCTCCAGAGAACTCAGAGTATGATGTTTCCAGCAAAACAGACATC 1028
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901 CTGGAAACCTTGGAAACGGCACGCTCTCCAGTACTGGAGGGCCAAAGCCCTGGCTG 960
1028
1029 CTGGAAACCTTGGAAACGGCACGCTCTCCAGTACTGGAGGGCCAAAGCCCTGGCTG 1088
1088
961 GTCTGTGTACACACAGAGCCCTCCAGCCAGGCTGAGCTGGACCCAGAGGGACAGGTT 1020
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1089 GTCTGTGTACACACAGAGCCCTCCAGCCAGGCTGAGCTGGACCCAGAGGGACAGGTT 1148
1088
1021 CTGAGCCCTCCAGCCCTCAGACCCGGGTCTCTGAGCTGGCTGGGTTCAGTGGAG 1080
1148
1149 CTGAGCCCTCCAGCCCTCAGACCCGGGTCTCTGAGCTGGCTGGGTTCAGTGGAG 1208
1081 CACGAAGGAGATTCACTGCGAGCTCGGACCCACTGGGCTCCAGCAGCTCTCTCTC 1140
1209 CACGAAGGAGATTCACTGCGAGCTCGGACCCACTGGGCTCCAGCAGCTCTCTCTC 1268
1141 AGCTCTCCGTGACTACTCCCCGAAGCTGTGGGCCCCCTCTCTCTCTGGAGGCTGAG 1200
1269 AGCTCTCCGTGACTACTCCCCGAAGCTGTGGGCCCCCTCTCTCTCTGGAGGCTGAG 1284
1201 GGTCTGCACTGCACTGTCTCTCCAGGCGAGCCCGGCCCTCTCTCTCTGGTGGCTT 1260
1285 ----- 1284
1261 GGGAGGAGTGTGTGGAGGGGAACAGCAGCCAGGACTCTCTTCGAGGTCACCCCAGCTCA 1320
1285 ----- 1284
1321 GCCGGGCCCTGGGCCAACAGCTCTCTGAGCTCTCATGGAGGGCTCAGCTCCGGCCTCAGG 1380
1285 ----- 1284
1381 CTCGGCTGTGAGGCTGGAACGTCTCATGGGCCCCAGAGTGATCTCTCTCAGCTGCCA 1440
1285 ----- 1284
1441 GATGAAGGAGGACTCATCTCAAGGCAATCTCAACGGAGGTTCTTGGGAATCGGCATC 1500
1285 -ATAAGAGGAGGACTCATCTCAAGGCAATCTCAACGGAGGTTCTTGGGAATCGGCATC 1343
1501 ACGGCTCTTCTTTCTCTGCTGGCCCTGATCATCATGAAGATTCTACCGAAGAGACGG 1560
1344 ACGGCTCTTCTTTCTCTGCTGGCCCTGATCATCATGAAGATTCTACCGAAGAGACGG 1403
1561 ACTCAGACAGAAACCCGAGCCAGGTTCTCCGGGACAGCAGATCTCTGGATTACATC 1620
1404 ACTCAGACAGAAACCCGAGCCAGGTTCTCCGGGACAGCAGATCTCTGGATTACATC 1463
1621 AATGTGTCCGAGGGTGGGCCCTCTGGCTCAGAAAGCGGAATCAGAAAGCCACACCAAC 1680

1464 AATGTGTCCGACGGCTGGCCCTCTGGCTCAGAAAGCGGAATCAGAAAGCCACACCAAC 1523
1681 AGTCTCTCGAGCCCTCTTCCACAGGTCTCTCTCCAGAAATCAAGAAAGAACAGAAA 1740
1524 AGTCTCTCGAGCCCTCTTCCACAGGTCTCTCTCCAGAAATCAAGAAAGAACAGAAA 1583
1741 AAGCAGTATCAGTTGCTCCAGTTTCCAGAAACCCAAATCATCCACTCAAGCCCGAGATCC 1800
1584 AAGCAGTATCAGTTGCTCCAGTTTCCAGAAACCCAAATCATCCACTCAAGCCCGAGATCC 1643
1801 CAGGAGAGCCAGAGGAGCTCCATTATGCCAGGTCTCACTTCCAGGGGCTCAGACCCAGG 1860
1644 CAGGAGAGCCAGAGGAGCTCCATTATGCCAGGTCTCACTTCCAGGGGCTCAGACCCAGG 1703
1861 CCTGAGGCCCGGATGCCAAAGGGCAACCCAGGGGGAATATGAGAAAGTCAAGTTCAA 1917
1704 CCTGAGGCCCGGATGCCAAAGGGCAACCCAGGGGGAATATGAGAAAGTCAAGTTCAA 1760

Search completed: November 8, 2004, 09:33:29
Job time : 1333.86 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2004, 13:50:18 ; Search time 112.542 Seconds
(without alignments)
2617.614 Million cell updates/sec

Title: US-09-937-636-3
Perfect score: 2705
Sequence: 1 MLLPILLSLLGGSQMDGR.....RPEARMPKGTQADYAEVXFQ 512

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2576.5	95.2	697	1	SILA_HUMAN	Q961c7 homo sapien
2	2265	83.7	544	2	Q6UXI8	Q6uxi8 homo sapien
3	2265	83.7	544	2	AAQ88703	AaQ88703 homo sapi
4	2185	80.7	425	2	BAC85493	Bac85493 homo sapi
5	1513.5	55.9	686	1	SILB_HUMAN	Q961x6 homo sapien
6	1343.5	49.6	688	2	Q80ZE3	Q80ze3 mus musculu
7	1211.5	44.8	623	2	Q8BYI8	Q8byi8 mus musculu
8	955	35.3	499	2	Q7Z728	Q7z728 homo sapien
9	947	35.0	499	1	SIL8_HUMAN	Q9nyz4 homo sapien
10	909	33.6	595	1	SILL_HUMAN	Q96pq1 homo sapien
11	909	33.6	597	1	SILL_PANTR	Q951h0 pan troglod
12	878	32.4	468	2	Q6RJ50	Q6pj50 mus musculu
13	878	32.4	468	2	AAQ79834	AaQ79834 mus muscu
14	878	32.4	468	2	AAQ72479	AaQ72479 mus muscu
15	878	32.4	468	2	AAH23280	AaH23280 mus muscu
16	873	32.3	467	1	SIL5_MOUSE	Q91y57 mus musculu
17	870	32.2	463	1	SIL9_HUMAN	Q9y336 homo sapien
18	861	31.8	439	2	Q6GTU4	Q6gtu4 homo sapien
19	836	30.9	442	1	SIL5_HUMAN	Q43599 homo sapien
20	832.5	30.8	467	1	SILL_HUMAN	Q9y286 homo sapien
21	804.5	29.7	551	1	SIL5_HUMAN	O15389 homo sapien
22	796.5	29.4	551	2	AAH29896	AaH29896 homo sapi
23	792	29.3	394	2	Q6UXG0	Q6uxg0 homo sapien
24	792	29.3	394	2	AAQ88735	AaQ88735 homo sapi
25	787	29.1	437	2	AAH35359	AaH35359 homo sapi
26	698	25.8	364	2	CAD36503	Cad36503 homo sapi
27	694	25.6	364	1	CD33_HUMAN	P20138 homo sapien
28	689.5	25.5	569	1	SILF_MOUSE	Q920g3 mus musculu
29	664	24.5	269	2	Q8BTG2	Q8btg2 mus musculu
30	625	23.1	523	2	Q80ZE2	Q80ze2 mus musculu
31	530.5	19.6	304	2	Q81W38	Q81w38 homo sapien

RESULT 1

ID	SILA_HUMAN	STANDARD;	PRT;	697 AA.
AC	Q96LC7; Q96G54; Q96LC8;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Sialic acid binding Ig-like lectin 10 precursor (Siglec-10) (Siglec-like protein 2).			
GN	Name=SIGLEC10; Synonyms=SLG2;			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_taxID=9606;			
RN	[1]_taxID=9606;			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RX	MEDLINE=21303047; PubMed=11409878; DOI=10.1006/bbrc.2001.5053;			
RA	Yousef G.M., Ordon M.H., Fousias G., Diamandis E.P.;			
RT	"Molecular characterization, tissue expression, and mapping of a novel Siglec-like gene (SLG2) with three splice variants.";			
RL	Biochem. Biophys. Res. Commun. 284:900-910(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Spleen;			
RA	Munday J., Kerr S., Ni J., Cornish A.L., Zhang J.Q., Nicoll G.,			
RT	Floyd H., Mattei M.-G., Moore P., Liu D., Crocker P.R.;			
PT	"Identification, characterization and leucocyte expression of Siglec-10, a novel human sialic acid-binding receptor.";			
RL	Biochem. J. 355:489-497(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	TISSUE=Dendritic cell;			
RA	Li N., Zhang W., Wan T., Zhang J., Chen T., Yu Y., Wang J., Cao X.;			
RT	"Cloning and characterization of Siglec-10, a novel sialic acid binding member of the Ig superfamily, from human dendritic cells.";			
RL	J. Biol. Chem. 276:28106-28112(2001).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 3), ALTERNATIVE SPLICING (ISOFORMS 4 AND 5), MUTAGENESIS OF TYR-667, AND INTERACTION WITH PTPN6.			
RX	MEDLINE=21359381; PubMed=11358961; DOI=10.1074/jbc.M100467200;			
RA	Kitzing F., Martinez-Barriocanal A., Lopez-Botet M., Sayos J.;			
RT	"Cloning of two new splice variants of Siglec-10 and mapping of the interaction between Siglec-10 and SHP-1.";			
RL	Biochem. Biophys. Res. Commun. 296:355-362(2002).			
RN	[5]			
RP	SEQUENCE OF 337-697 FROM N.A. (ISOFORM 1/3/4).			
RC	TISSUE=B-cell;			
RX	MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RT	Klausberg R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,			
RL	Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Raha S.S., Joquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. Preferentially binds to alpha2,3- or 2,6-linked sialic acid. The sialic acid recognition site may be masked by cis interactions with sialic acids on the same cell surface. In the immune response, may act as an inhibitory receptor upon ligand induced tyrosine phosphorylation by recruiting cytoplasmic phosphatase(s) via their SH2 domain(s) that block signal transduction through dephosphorylation of signaling molecules.

CC -!- SUBUNIT: Interacts with PTPN6/SHP-1 upon phosphorylation.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1-4); secreted (isoform 5).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=5;

CC Name=1; Synonyms=Long;

CC IsoId=Q961C7-1; Sequence=Displayed;

CC Name=2; Synonyms=Short, Sv1;

CC IsoId=Q961C7-2; Sequence=VSP_002565;

CC Name=3; Synonyms=SV3;

CC IsoId=Q961C7-3; Sequence=VSP_002564;

CC Name=4; Synonyms=SV4;

CC IsoId=Q961C7-4; Sequence=VSP_002561;

CC Name=5; Synonyms=SV2;

CC IsoId=Q961C7-5; Sequence=VSP_002562, VSP_002563;

CC -!- TISSUE SPECIFICITY: Expressed by peripheral blood leukocytes (eosinophils, monocytes and a natural killer cell subpopulation). Isoform 5 is found to be the most abundant isoform. Found in lymph node, lung, ovary and appendix. Isoform 1 is found at high levels and isoform 2 at lower levels in bone marrow, spleen and spinal chord. Isoform 2 is also found in brain. Isoform 4 is specifically found in natural killer cells.

CC -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in modulation of cellular responses. The phosphorylated ITIM motif can bind the SH2 domain of several SH2-containing phosphatases.

CC -!- PTM: Phosphorylation of Tyr-667 is involved in binding to PTPN6.

CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC (sialic acid binding Ig-like lectin) family.

CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

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DR ENBL; AY029277; AAK40255.1; -

DR ENBL; AY029277; AAK40256.1; -

DR ENBL; AF310233; AAK55139.1; -

DR ENBL; AF311905; AAK92542.1; -

DR ENBL; AY032685; AAK51124.1; -

DR ENBL; BC009955; AAK09955.2; -

DR HSSP; Q9Y286; 1075.

DR Genew: HGNC:15620; SIGLEC10.

DR MIM: 606091; -

DR InterPro: IPR007110; Ig-like.

DR InterPro: IPR003598; Ig_C2.

DR InterPro: IPR003006; Ig_MHC.

DR Pfam: PF00047; Ig_3.

DR SMART: SM00408; IGC2; 2.

DR PROSITE: PS00835; IG LIKE; 3.

DR PROSITE: PS00290; IG_MHC; 1.

KW Alternative splicing; Cell adhesion; Glycoprotein.

KW Immunoglobulin domain; Lectin; Phosphorylation; Repeat; Signal; Transmembrane.

FT SIGNAL 1 16 Potential.

FT CHAIN 17 697 Sialic acid binding Ig-like lectin 10.

FT DOMAIN 17 550 Extracellular (Potential).

FT TRANSMEM 551 571 Potential.

FT DOMAIN 572 697 Cytoplasmic (Potential).

FT DOMAIN 18 121 Ig-like V-type.

FT DOMAIN 146 231 Ig-like C2-type 1.

FT DOMAIN 251 339 Ig-like C2-type 2.

FT DOMAIN 344 441 Ig-like C2-type 3.

FT SITE 595 600 ITIM motif 1.

FT SITE 655 670 ITIM motif 2.

FT DISULFID 36 173 By similarity.

FT DISULFID 41 101 By similarity.

FT DISULFID 164 215 By similarity.

FT DISULFID 276 323 By similarity.

FT DISULFID 380 425 By similarity.

FT MOD_RES 667 667 Phosphotyrosine.

FT CARBOHYD 100 100 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 355 355 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 364 364 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 486 486 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 504 504 N-linked (GlcNAc...) (Potential).

FT VARSPLIC 125 214 Missing (in isoform 4).

FT VARSPLIC 140 185 Missing (in isoform 5).

FT VARSPLIC 186 697 Missing (in isoform 5).

FT VARSPLIC 141 198 Missing (in isoform 3).

FT VARSPLIC 445 539 Missing (in isoform 2).

FT MUTAGEN 667 Y->F: Abolishes binding to PTPN6.

FT CONFLICT 28 28 S -> P (in Ref. 4).

FT CONFLICT 134 134 G -> R (in Ref. 4).

FT CONFLICT 226 226 V -> A (in Ref. 1).

FT CONFLICT 344 344 P -> S (in Ref. 3).

FT CONFLICT 440 440 L -> P (in Ref. 4).

FT CONFLICT 587 587 R -> K (in Ref. 3).

FT CONFLICT 625 625 P -> S (in Ref. 3).

SQ SEQUENCE 697 AA; 76619 MW; 6CB231CE49411D18 CRC64;

Query Match 95.2%; Score 2576.5; DB 1; Length 697;

Best Local Similarity 73.0%; Pred. No. 3.9e-167;

Matches 509; Conservative 1; Mismatches 2; Indels 185; Gaps 2;

QY 1 MLLPLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSPYPRQDTGTPAYGYW 60

DB 1 MLLPLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSPYPRQDTGTPAYGYW 60

QY 61 PKATETTKGAPVATNQHOSREVENSTGRFQLTGDPKAGNCSLVIRDAQWDSQYEFVR 120

DB 61 PKATETTKGAPVATNQHOSREVENSTGRFQLTGDPKAGNCSLVIRDAQWDSQYEFVR 120

QY 121 ERGSYVRYNFMNDGFFLKVTALTKQDPVYIPETLEPQGPVTVICVFNWAFEECPFPFSW 180

DB 121 ERGSYVRYNFMNDGFFLKVTALTKQDPVYIPETLEPQGPVTVICVFNWAFEECPFPFSW 180

QY 181 TGAALSSQGTPTTSHSFVSFTFPRPDHDTDLTCHVDFSRKGVSAQRTVLRVAYAPRD 240

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Db 181 TGAALSSQGTPTTSHFVLSFTPRPDHNTDLTCHVDTSKGVSVQRTVRLAVAYAPD 240
QY 241 LVISISRDNTPD----- 252
Db 241 LVISISRDNTPALEPOFGNVPYLEAKQGFLLCAADSQPPATLSWVLQNRVLSSSH 300
QY 253 ----- 360
Db 301 WGPRLGLELPGVKAGDSGRYTCRAENRLGSGQRAALDLSVQYPPENLRVMVSOANRTVLE 360
QY 271 NLNGTSLPVLGOSLCLVCTHSSPPARLSWTORGQVLSPPSPQSPGVLELPRVQVEHE 330
Db 361 NLNGTSLPVLGOSLCLVCTHSSPPARLSWTORGQVLSPPSPQSPGVLELPRVQVEHE 420
QY 331 GEFTCHARHPLGSOHVSLSLVHY----- 354
Db 421 GEFTCHARHPLGSOHVSLSLVHYSPKLLGPSCSWEAGHLHCSCSQASPAPSLRWLGE 480
QY 355 -----X 355
Db 481 ELLEGNSQDSFEVTPSSAGFWANSSLSLHGGLSGRLRCEAWNVHGAQSGSILQLPDK 540
QY 356 KGLISTAFNSGAFGLGIGITALFLCALIIMTKILPKERTQETPRPRFSRHSTILDYINV 415
Db 541 KGLISTAFNSGAFGLGIGITALFLCALIIMTKILPKERTQETPRPRFSRHSTILDYINV 600
QY 416 VPTAGLAQRNOKATPNSPRTPLPPCAPSPESKQKQYQLPSPFPKSTQAPESOE 475
Db 601 VPTAGLAQRNOKATPNSPRTPLPPCAPSPESKQKQYQLPSPFPKSTQAPESOE 660
QY 476 SQBELHYATLNFPGVPRPEARMKGTQADYAEVKFQ 512
Db 661 SQBELHYATLNFPGVPRPEARMKGTQADYAEVKFQ 697
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RESULT 2

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Q6UX18 PRELIMINARY; PRT; 544 AA.
ID Q6UX18
AC Q6UX18
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE SIGLEC10.
GN O6FNames:UNQ477;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22857296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vasts A.,
RA Vanden R., Watanabe C., Wied D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR ENBL: AX358337; AQ088703.1; -.
DR InterPro: IPR003599; I9.
DR InterPro: IPR007110; I9-like.
DR InterPro: IPR003598; I9.c2.
DR InterPro: IPR003006; I9_MHC.
DR Pfam: PF00047; I9; 2.
DR SMART: SM00409; I9; 3.
DR SMART: SM00408; I9c2; 2.
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DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 544 AA; 60267 MW; 4D84B1EF6D60AC8CB CRC64;
Query Match 83.7%; Score 2265; DB 2; Length 544;
Best Local Similarity 74.8%; Pred. No. 4.8e-146;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;
QY 1 MLLPLLSSLLGSGQAMDGRFWIRVOESVMVPEGICISVPCSFSPRODWTGSTPAYGVW 60
Db 1 MLLPLLSSLLGSGQAMDGRFWIRVOESVMVPEGICISVPCSFSPRODWTGSTPAYGVW 60
QY 61 FKAVTETTKGAPVATNHQSRREVEMSTRGRFOLTGDPAKGNCSLVIRDAQMDESQYFFRV 120
Db 61 FKAVTETTKGAPVATNHQSRREVEMSTRGRFOLTGDPAKGNCSLVIRDAQMDESQYFFRV 120
QY 121 ERGSVVRVNFWDGFFLVLTALTQKPDYVIETLEPGQPVTVICVFNWAFEECPPPSPW 180
Db 121 ERGSVTVTNFWDGFFLVLT----- 140
QY 181 TGAALSSQGTPTTSHFVLSFTPRPDHNTDLTCHVDTSKGVSAQRTVRLVAYAPD 240
Db 141 -----VLSFTPRPDHNTDLTCHVDTSKGVSAQRTVRLVAYAPD 182
QY 241 LVISISRDNTPD----- 252
Db 183 LVISISRDNTPALEPOFGNVPYLEAKQGFLLCAADSQPPATLSWVLQNRVLSSSH 242
QY 253 -----PPENLVRMVSOANRTVLE 270
Db 243 WGPRLGLELPGVKAGDSGRYTCRAENRLGSGQRAALDLSVQYPPENLRVMVSOANRTVLE 302
QY 271 NLNGTSLPVLGOSLCLVCTHSSPPARLSWTORGQVLSPPSPQSPGVLELPRVQVEHE 330
Db 303 NLNGTSLPVLGOSLCLVCTHSSPPARLSWTORGQVLSPPSPQSPGVLELPRVQVEHE 362
QY 331 GEFTCHARHPLGSOHVSLSLVHYKKGILSTAFNGAFLGIGITALFLCALIIMTKILP 390
Db 363 GEFTCHARHPLGSOHVSLSLVHYKKGILSTAFNGAFLGIGITALFLCALIIMTKILP 422
QY 391 KRTQTETPRPRFSRHSTILDYINVVPTAGLAQRNOKATPNSPRTPLPPCAPSPESK 450
Db 423 KRTQTETPRPRFSRHSTILDYINVVPTAGLAQRNOKATPNSPRTPLPPCAPSPESK 482
QY 451 NQKQYQLPSPFPKSTQAPESQBELHYATLNFPGVPRPEARMKGTQADYAEVK 510
Db 483 NQKQYQLPSPFPKSTQAPESQBELHYATLNFPGVPRPEARMKGTQADYAEVK 542
QY 511 FQ 512
Db 543 FQ 544
RESULT 3
AAQ88703 PRELIMINARY; PRT; 544 AA.
ID AAQ88703
AC AAQ88703
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE SIGLEC10.
GN UNQ477.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
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Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
 Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 Godowski P.;
 "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
 Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
 Bioinformatics Assessment";
 Genome Res. 13:2265-2270(2003).
 DB EMBL: AY358337; AAC88703.1; -
 SO SEQUENCE 544 AA; 60267 MW; 4DA4E1EF6D6AC8CB CRC64;
 Query Match 83.7%; Score 2265; DB 2; Length 544;
 Best Local Similarity 74.8%; Pred. No. 4.9e-146;
 Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;
 1 MLPLLLSSLLGGSOAMDGRFWIRVQESVMPVPEGLCLISVPCSFSPYPRQDWTGSTPAYGW 60
 1 MLPLLLSSLLGGSOAMDGRFWIRVQESVMPVPEGLCLISVPCSFSPYPRQDWTGSTPAYGW 60
 61 FKAVTTTKGAPVATNHNOSREVMSTGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
 61 FKAVTTTKGAPVATNHNOSREVMSTGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
 121 ERGSYVYVFNWMDGFLKVTALTQKPDVYIPETLEPQPVTVICVFNWAFECPPPSFW 180
 121 ERGSYVYVFNWMDGFLKVTALTQKPDVYIPETLEPQPVTVICVFNWAFECPPPSFW 180
 181 TGAALSSQGTGKPTTSHFSVLSFTPRQDHTDLTCHVDFSRKGVSAQRTVLRVAVAPRD 240
 141 -----VLSFTPRQDHTDLTCHVDFSRKGVSAQRTVLRVAVAPRD 182
 241 LVISISRDNTPD----- 252
 183 LVISISRDNTPALEPQPGQNVPLYEAQKGFRLRLCAADSPATLSWLVQNRVLSSSH 242
 253 -----PPENLRVWVMSQANRTVLE 270
 243 WGRPLGLEPLGVKAGSGRYTCAENRLOSQQRALDLSVOYPPENLRVWVMSQANRTVLE 302
 271 NLNGTSLPVLGOSLCLVCTHSSPPARLSWTQRGVLSPPSPDPSDGVLELPRVQVEH 330
 303 NLNGTSLPVLGOSLCLVCTHSSPPARLSWTQRGVLSPPSPDPSDGVLELPRVQVEH 362
 331 GEFTCHARHPLGSHVLSLVHYKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP 390
 363 GEFTCHARHPLGSHVLSLVHYKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP 422
 391 KRRTQTETPRFRSHSTILDYINVVPTAGLACKNOKATPNSPRTPLPPGAPSPESKK 450
 423 KRRTQTETPRFRSHSTILDYINVVPTAGLACKNOKATPNSPRTPLPPGAPSPESKK 482
 451 NQKQYQLPSPFPKSTQAPESQSEELHYATLNPFGVPRPEAMPKGTQADYAEVK 510
 483 NQKQYQLPSPFPKSTQAPESQSEELHYATLNPFGVPRPEAMPKGTQADYAEVK 542
 511 FQ 512
 543 FQ 544

RESULT 4

ID BAC85493 PRELIMINARY; PRT; 425 AA.
 AC BAC85493;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DE CDNA FLJ16033 fis, clone SPLEN2001599, weakly similar to Homo sapiens
 DE sialic acid binding immunoglobulin-like lectin 8 long splice variant
 DE (Siglec8) gene.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

RESULT 5

ID SILB HUMAN STANDARD; PRT; 686 AA.
 AC Q96RL6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Sialic acid binding Ig-like lectin 11 precursor (Siglec-11) (Sialic
 DE acid-binding lectin 11) (UNQ9222/PRO28718).
 GN Name=SIGLEC11;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
 OX NCBI TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Splice;
 RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
 Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
 Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
 Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
 Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
 Wagatsuma M., Murakawa K., Kurehori K., Takahashi-Fujii A., Oshima A.,
 Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
 Masuho Y., Nagai K., Isogai T.;
 RA "NEO human cDNA sequencing project";
 RT Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK122619; BAC85493.1; -
 KW Lectin.
 SQ SEQUENCE 425 AA; 47345 MW; 809854127B397D73 CRC64;

Query Match 80.7%; Score 2185; DB 2; Length 425;
 Best Local Similarity 87.2%; Pred. No. 1e-140;
 Matches 421; Conservative 2; Mismatches 2; Indels 58; Gaps 1;
 30 MVPEGLCLISVPCSFSPYPRQDWTGSTPAYGWFKAVTTTKGAPVATNHNOSREVMSTGR 89
 1 MVPEGLCLISVPCSFSPYPRQDWTGSTPAYGWFKAVTTTKGAPVATNHNOSREVMSTGR 60
 90 FQLTGDPKAGNCSLVIRDAQMDESQYFFRVVYVFNWMDGFLKVTALTQKPDVY 149
 61 FQLTGDPKAGNCSLVIRDAQMDESQYFFRVVYVFNWMDGFLKVT----- 111
 150 IPETLEPQPVTVICVFNWAFECPPPSFMTGAALSSQGTGKPTTSHFSVLSFTPRQDH 209
 112 -----VLSFTPRQDH 122
 210 DTLTCHVDFSRKGVSAQRTVLRVAVAPRDVLISISRDNTPDPPENLRVWVMSQANRTVL 269
 123 NDTLTCHVDFSRKGVSAQRTVLRVAVAPRDVLISISRDNTPDPPENLRVWVMSQANRTVL 182
 270 ENLNGTSLPVLGOSLCLVCTHSSPPARLSWTQRGVLSPPSPDPSDGVLELPRVQVEH 329
 183 ENLNGTSLPVLGOSLCLVCTHSSPPARLSWTQRGVLSPPSPDPSDGVLELPRVQVEH 242
 330 EGFTCHARHPLGSHVLSLVHYKGLISTAFSNGAFLGIGITALLFLCLALIIMKIL 389
 243 EGFTCHARHPLGSHVLSLVHYKGLISTAFSNGAFLGIGITALLFLCLALIIMKIL 302
 390 KRRTQTETPRFRSHSTILDYINVVPTAGLACKNOKATPNSPRTPLPPGAPSPESK 449
 303 KRRTQTETPRFRSHSTILDYINVVPTAGLACKNOKATPNSPRTPLPPGAPSPESK 362
 450 NQKQYQLPSPFPKSTQAPESQSEELHYATLNPFGVPRPEAMPKGTQADYAEV 509
 363 NQKQYQLPSPFPKSTQAPESQSEELHYATLNPFGVPRPEAMPKGTQADYAEV 422
 510 KQF 512
 423 KQF 425


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365 -----NGAFLGIGITALLFLCLALIMKILPKRTTOTETPRPRSRHSTILDYINNVPE 417
QY |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 542 EHGGGLGALGNGVALLAFSLVVFVKCRK-----EAKRAAEQ-----DVPS 591
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 418 TAGPLAQRNOKATPNSPRPLPGAPSPSKKNOKQYOLPSPFKSTQAPESQEQ 477
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 592 TLGPISQGHQESAGSSQDHPPGA-----ATYFGKGEQ 628
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 478 EELHYATLNPFGVPRPEARMKGTQADYAEVK 510
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 629 -ELHYASLSFQGLRWEPADQAPSTTEYSEIK 660
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 6
DB 360Z33 PRELIMINARY; PRT; 688 AA.
AC Q80ZE3
DB 01-JUN-2003 (TREMELrel. 24, Created)
DB 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DB 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DB Siglec-G.
DB Name=Siglec10;
DB Mus musculus (Mouse);
DB Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DB Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
DB NCBI_TaxID=10090;
DB [1]
DB SEQUENCE FROM N.A.
DB STRAIN=BALB/c;
DB MEDLINE=22921108; PubMed=14559209;
DB Alzawa H., Zimmermann N., Carrigan P.E., Lee J.J., Rothenberg M.E.,
DB Bochner B.S.;
DB "Molecular analysis of human Siglec-8 orthologs relevant to mouse
DB eosinophils: identification of mouse orthologs of Siglec-5 (mSiglec-F)
DB and Siglec-10 (mSiglec-G)";
DB Genomics 82:521-530(2003).
DB EMBL; AY210400; AA048273.1; -
DB HSP; Q9F286; 107S.
DB MGD; MGI:2443630; Siglec10.
DB InterPro; IPR007110; Ig-like.
DB InterPro; IPR003598; Ig_c2.
DB Pfam; PF00047; Ig; 2.
DB SMART; SM00408; IGc2; 2.
DB PROSITE; PS00835; IG_LIKE; 3.
DB SEQUENCE 688 AA; 76884 MW; 21A619E1500BFA76 CRC64;

Query Match 49.6%; Score 1343.5; DB 2; Length 688;
Best Local Similarity 43.0%; Pred. No. 4.2e-83;
Matches 297; Conservative 67; Mismatches 138; Indels 189; Gaps 10;

QY 2 LLPFLLSLGGQAMGRWIRVOESVYVMPGELISVPCSFYPRQDWTGSTPAYGYWF 61
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 3 LLPFLSFLDGGPGQWESYFLOQRVKAQEGELCIFVPCSFSPGKMLNRSPLGYWF 62
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 62 KAVTETTKGAPVATNHQSREVENSTRGRFQLTGDPKAGNCSLVIRDAQMDQESQYFFRYE 121
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 63 KGIRKPSLFPVATNKKVLENEARGFOLLGDISKKNCSLLIKDVQWGDSTNYFFRYE 122
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 122 RGSVRYNPNNDGFLKVTALTQKPDVVIETLEPGQPVTVICVFWWAECECPSPFSWT 181
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 123 RG-FERESFKEE-FRLQVEALTQKPDIFIEVLEPGEPVFWCLFQWTFNQCPAPFSWM 180
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 182 GAALSSGKTPTTSHFVSLGFTPRAPQCHDLDLTCHVDPSRKGVSAQTVKRLRVAVAPRDL 241
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 181 GDVAFSFBSPHTSNYSVLFSFIPQLQHDHDLTCQLDFSR--NSTQETVRLRVAYAPRSL 238
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 242 VISISRNN--TPD----- 252
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 239 AISIFHDNVSPDLHENPSHLEVQGGQSLRLCTADSPATLSWLVLEDQVLSWSSPVGS 298
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 253 -----PPENLRVWVSQANVTLENLG 273
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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DB 239 RTLALELPMWKAGSGHYTCQAEMLRSGQHTLDLSVLYPPQDLRVTVTSQANRTVLILR 358
QY |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 274 NQTSPLVLEGOSLCLVCTHSSPARLSWTQRGQVLSPSQSPDQVLELPRVQVHEHGEF 333
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 359 NALSPLVLEGOSLCLVCTYSNPPANVSAMVWVTTLIPIQSSEPGVLELPIVQREHGEF 418
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 334 TCHARHPGSGHVSLSLSVHY-----KKGL----- 358
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 419 TCAAQNPAGQRIISLSLSVHYPPQMSFSPSCWEAKGLHCNCSRAWPAPSLRWLGRGLL 478
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 359 -----IS 360
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 479 EGNSSNASFTVTFSSLGPWNSSLSLQELGPSLWSCSNWTHGAQTTSVLLLPDKDSA 538
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 361 TAFSNGAFLGIGITALLFLCLALIMKILPKRTTOTETPRPRSRHSTILDYINNVPTAG 420
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 539 TAFSGAVLFGITALLALCLIVIVIKTLQKKGTOEPPSRPKLSRGSTILYINNVPKTR 598
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 421 PLAQRNOKATPNSPRPLPGAPSPSKKNOK-KQYOLPSPFKSTQAPESQEQ 479
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 599 SLA--RNWKAEPDAPSKSSPLDTHFPKPKKQKDPHFTYPCPDPTSSSQVPSNNPPEE 656
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 480 LHYATLNPFGVPRPEARMKGTQADYAEVK 510
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 657 LHYAALNPSRLRLQ-ETODPDQDTSYSDTEVR 686
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 7
Q8BY18 PRELIMINARY; PRT; 623 AA.
AC Q8BY18;
DB 01-MAR-2003 (TREMELrel. 23, Created)
DB 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DB 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DB Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
DB library, clone: A630096C01 product: weakly similar to SIALIC ACID-
DB BINDING LECTIN (Fragment).
DB Name=Siglec10;
DB Mus musculus (Mouse);
DB Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DB Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
DB NCBI_TaxID=10090;
DB [1]
DB SEQUENCE FROM N.A.
DB STRAIN=C57BL/6J; TISSUE=Thymus;
DB MEDLINE=98279253; PubMed=10349636;
DB Carninci P., Hayashizaki Y.;
DB "High-efficiency full-length cDNA cloning.";
DB Meth. Enzymol. 303:19-44(1999).
DB [2]
DB SEQUENCE FROM N.A.
DB STRAIN=C57BL/6J; TISSUE=Thymus;
DB MEDLINE=21085660; PubMed=11217851;
DB RIKEN FANTOM Consortium;
DB "Functional annotation of a full-length mouse cDNA collection.";
DB Nature 409:685-690(2001).
DB [3]
DB SEQUENCE FROM N.A.
DB STRAIN=C57BL/6J; TISSUE=Thymus;
DB The FANTOM Consortium;
DB the RIKEN Genome Exploration Research Group Phase I & II Team;
DB "Analysis of the mouse transcriptome based on functional annotation of
DB 60,770 full-length cDNAs.";
DB Nature 420:563-573(2002).
DB [4]
DB SEQUENCE FROM N.A.
DB STRAIN=C57BL/6J; TISSUE=Thymus;
DB MEDLINE=20499374; PubMed=11042159;
DB Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
DB Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
DB "Normalization and subtraction of cap-trapper-selected cDNAs to
DB prepare full-length cDNA libraries for rapid discovery of new genes.";
DB Genome Res. 10:1617-1630(2000).
DB [5]

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RN RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohata E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RA "AIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
RN RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitho H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK042488; BAC31272.1;
DR HSSP; Q9Y285; 1078.
DR MGD; MGI:2443630; Siglec10.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:hemophilic cell adhesion; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGG2; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
KW Lectin.
FT NON TER 623 623
SQ SEQUENCE 623 AA; 69384 MW; 5827C09D52C3AC7F CRC64;

Query Match 44.8%; Score 1211.5; DB 2; Length 623;
Best Local Similarity 43.8%; Pred. No. 3.7e-74;
Matches 267; Conservative 55; Mismatches 111; Indels 187; Gaps 8;

QY 2 LLEPLLSLLGSGQAMDGFRWIRVQSVVMVPEGLCISVPCFSYPRQDWGTSTPAYGYWF 61
Db 3 LLLFLLSFLLDGPQGQMSYFLQVQIRVKAQGLCIFVPCFSPPSGKWLNRSPLYGYWF 62
QY 62 KATETTKGAPVATNQHSEVENSTGRFQLTCDPAKGNCSLVIRDAQMDSQYFFRVE 121
Db 63 KGIKPSLSFPVATNKKVLEAEAGRFQLLDISKKNCSLLIKDVQGDSTNYFFRVE 122
QY 122 RGSYVRNFMNDGFFLKVLTALTKQPVYIPETLEPGQPVTVICVFNWAEFCPPPSFSWT 181
Db 123 RG-FERFSPEE-FRLQVEALTQKPIFIPVLEPGEPVTVVCLFSWTNQCPSPFSWM 180
QY 182 GAALSSCGTKPTTSHSVLSFTPRPODHDILTCHVDPRKGVSAQRTVRLRVAYAPRDL 241
Db 181 GDAVSQESRPHSTSNYSVLSPFGLQHDHTELTCLQDFSR--MSTQRTVRLRVAYAPRSL 238
QY 242 VISISDN--TPD----- 252
Db 239 AISIFHDNVSVDLHNPENSHLEVVQQQSURLLCTADSQPPALSLWLEQVLSWSFVGS 298
QY 253 -----PPENLRVMVQANRTVLENLG 273
Db 299 RTLALSLPVMKAGDSGHYTCQAEENRLGSQQHTLDLSVLPQDRLRVTVSCANRTVLEILR 358
QY 274 NGTSLPVLGOSLCIVCTHSSPRLSWTQROVLSPQSPDPGVLELPRVQVEHEGEF 333

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Db 359 NAISLPVLGOSLCIVCTYSNPPANVSWAVVTQTLPIQSSEPGVLELPLVQREHEGEF 418
QY 334 TCHARRHPLGSOHVSLSLVHY-----KKGLE----- 358
Db 419 TCAQNPLGAORISLSLSVHYPPQWSSPSCSWKAGLHCNCSSRAWPAPSLRWLREGLL 478
QY 359 -----IS 360
Db 479 EGNSSNASFTVFSSGLGPNWNSLSLQELGSLWLSCESNWTHGAQTTSVLLLPDKDSA 538
QY 361 TAFNSGAFGLGITALFLCALILMILPKRQOTETPRPRFSRHSHTILDYINVVPTAG 420
Db 539 TAFSKGAVLGFITALLALCLIVIVTKLQKGTQEBSPRPKLSRGSTILDIYINVVPR 598
QY 421 PLAQRNOKATPNSPRTPPLP 440
Db 599 SLA--RNWKAEPDAPSRSSP 616

RESULT 8
Q72728 PRELIMINARY; PRT; 499 AA.
ID Q72728 AC Q72728;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haeh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.I., Scheetz T.E.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
SEQUENCE FROM N.A.
RP TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053319; AAH53319.1;
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGG2; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Hypothetical protein.
SQ SEQUENCE 499 AA; 54052 MW; CA32FEF7A88A7D3D CRC64;

Query Match 35.3%; Score 955; DB 2; Length 499;
Best Local Similarity 42.3%; Pred. No. 8.4e-57;
Matches 224; Conservative 70; Mismatches 160; Indels 76; Gaps 13;

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1  MLLPLLLSLLGSSQAMD-----RFWIRVQBSVMVPEGLCISVPCSFSPYRQDWTGST 54
2  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
3  1  MLLPLLLPULLMTGKMGEGDQYGDGVLQVQLVTVQEGLCVHVFCSPSPYQDGTSD 60
4  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
5  55  PAQYWFKAVETTKGAFVATNQHOSREVMSTGRQLGDPKAGKNSLVIRDAQNQDES 114
6  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
7  61  PVHGYWFRAGRPVQDAPVATNPNDRVQAEQCRFLQGLGDIWNSDCSIRDAKRDKG 120
8  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
9  115  QYPRVERGSY-----VRYNFMNDGFLPKVTALTQKPDVPIPTLEPGQPVTVICFVNW 169
10 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
11 121  SYFRLERGSWMKSYKQNLNKKQLSVFVTALTRPDILLTGLSGHPRNLTCSPVNA 180
12 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
13 170  FECCPPSPFWTGMALSSQGTKTTSFHSVLSPTTPRQDHTDLTCHVDPSRKGVSQRT 229
14 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
15 181  CKQGTTPMISWIGASVSPG--PTARSSVLTLPKPDQHGTLTQVTLPGTGVTTTST 238
16 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
17 230  VRLRVAVAPRDLVISIRDNTPPENLRVWVSOANRTVLENLNGTSTLPVLEGGQSLCLV 289
18 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
19 239  VRLDVSY-----PPWNLTVTVFQGDATASTALNGSSLSVLEGGQSLRLV 282
20 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
21 290  CVTHSSPPARLWTRQGVLSQPSQDPGVLELPRVQVHEGHEFTCHARHPLGSHVSUS 349
22 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
23 283  CAVNSNPARRLWTRGSLTLCPSRSSNFGLELPRVHVRDEGEFTCRAQNAQGSQHSIS 342
24 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
25 350  LSVHYKGLSTAFSN---GAFGIGITALLFL--GLALIMKILPKERTOTETPRPFS 404
26 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
27 343  LSLQNEGTGSRPVSQVTLAAVGAGATALAFUSFCIFIV-----RSCRKKSARPAAG 397
28 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
29 405  RHSTILSYINWV---PTAGPLAKRNKQATPNSPTPLPPEGAPSPSKNKKQYQLPSF 461
30 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
31 398  VGDIGMEDAKAIRGSAQGLPSTESKWD---GNELKPKPPAV-----435
32 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
33 462  PEPKSSQTQAESSESQELHYATLNPFGVTPR-PEARMKGTQADYAEVK 510
34 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
35 436  -----AFSSGE-EGELHYATLSLPHKVRPDPQFGQ--EATDSEYSEIX 474
36 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 9

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ID  SILE HUMAN STANDARD; PRT; 499 AA.
AC  Q9NYZ4;
DT  28-FEB-2003 (Rel. 41, Created)
DI  28-FEB-2003 (Rel. 41, Last sequence update)
DE  01-OCT-2004 (Rel. 45, Last annotation update)
DE  Sialic acid binding Ig-like lectin 8 precursor (Siglec-8)
DE  (Sialoadhesin family member-2) (SAP-2).
GN  Name=SIGLEC8; Synonyms=SAF2;
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A. (ISOFORM 1).
RX  MEDLINE=20549027; PubMed=11059593; DOI=10.1006/bbrc.2000.3866;
RA  Fousias G., Yousef G.M., Diamandis E.P.;
RA  D'Alessio K.J., Holmes S.D., Abrahamson J.A., Erickson-Miller C.L.,
RA  Murdoch P.R., Tachimoto H., Schleimer R.P., White J.R.;
RA  "Identification of SAP-2, a novel siglec expressed on eosinophils,
RA  mast cells, and basophils."
RA  J. Allergy Clin. Immunol. 105:1093-1100(2000).
RN  [3]
RP  SEQUENCE FROM N.A. (ISOFORM 3).
RX  MEDLINE=20314554; PubMed=10856141;
RA  Kikly K.K., Bochner B.S., Freeman S.D., Tan K.B., Gallagher K.T.,
RA  D'Alessio K.J., Holmes S.D., Abrahamson J.A., Erickson-Miller C.L.,
RA  Murdoch P.R., Tachimoto H., Schleimer R.P., White J.R.;
RA  "Identification of SAP-2, a novel siglec expressed on eosinophils,
RA  mast cells, and basophils."
RA  J. Allergy Clin. Immunol. 105:1093-1100(2000).
RN  [3]
RP  SEQUENCE FROM N.A. (ISOFORM 3).
RX  MEDLINE=20092847; PubMed=10625619;
RA  Floyd H., Ni J., Cornish A.L., Zeng Z., Liu D., Carter K.C., Steel J.,
RA  Crocker P.R.;

```

```

RT  "Siglec-8. A novel eosinophil-specific member of the immunoglobulin
RT  superfamily."
RL  J. Biol. Chem. 275:861-866(2000).
RN  [4]
RP  SEQUENCE FROM N.A. (ISOFORM 2).
RA  Floyd H., Zhang J.Q., Crocker P.R.;
RA  Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC  FUNCTION: Putative adhesion molecule that mediates sialic-acid
CC  dependent binding to cells. Preferentially binds to alpha2,3-
CC  linked sialic acid. Also binds to alpha2,6-linked sialic acid. The
CC  sialic acid recognition site may be masked by cis interactions
CC  with sialic acids on the same cell surface.
CC  SUBCELLULAR LOCATION: Type I membrane protein.
CC  ALTERNATIVE PRODUCTS:
CC  Event=Alternative splicing; Named isoforms=3;
CC  Name=1; Synonyms=Long;
CC  IsoId=Q9NYZ4-1; Sequence=Displayed;
CC  Name=2;
CC  IsoId=Q9NYZ4-2; Sequence=VSP_002559;
CC  Name=3;
CC  IsoId=Q9NYZ4-3; Sequence=VSP_002560;
CC  TISSUE SPECIFICITY: Expressed specifically on eosinophils.
CC  DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to
CC  as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This
CC  motif is involved in modulation of cellular responses. The
CC  phosphorylated ITIM motif can bind the SH2 domain of several SH2-
CC  containing phosphatases.
CC  SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
CC  (sialic acid binding Ig-like lectin) family.
CC  SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC  SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  EMBL; AF287892; AAC00573.1; -
CC  EMBL; AF223403; AAF34702.1; -
CC  EMBL; AF195032; AAF27622.1; -
CC  EMBL; AF310234; AAF55140.1; -
CC  HSP; O9Y286; 1078.
CC  Genew; HGNC:10877; SIGLEC8.
CC  MIM; 605639; -; C: integral to membrane; TAS.
CC  GO; GO:0016021; C: integral to membrane; TAS.
CC  GO; GO:0005529; F: sugar binding; TAS.
CC  GO; GO:0004888; F: transmembrane receptor activity; TAS.
CC  GO; GO:0007165; P: signal transduction; TAS.
CC  InterPro; IPR007110; IG-like.
CC  InterPro; IPR003598; IG_c2.
CC  Pfam; PF00047; Ig_2.
CC  SMART; SM00408; IGC2; 1.
CC  PROSITE; PS50835; IG_LIKE; 2.
CC  Alternative splicing; Cell adhesion; Glycoprotein;
CC  Immunoglobulin domain; Lectin; Repeat; Signal; Transmembrane.
FT  SIGNAL 1 16
FT  CHAIN 17 499
FT  DOMAIN 17 363
FT  TRANSMEM 364 384
FT  DOMAIN 385 499
FT  DOMAIN 40 123
FT  DOMAIN 157 240
FT  DOMAIN 246 344
FT  SITE 445 450
FT  SITE 468 473
FT  DISULFID 42 181
FT  DISULFID 47 107
FT  DISULFID 175 224
FT  DISULFID 283 328
FT  CARBOHYD 172 172

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FT CARBOHYD 249 249 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 267 245 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 152 245 ALTHRPDILIGLTLGSHSRNLQTCSPVPKQGTPTPMISWI
FT GASVSPGPTTARSSVLTLTPKPDQGTSLTCQVTLPGTV
FT TITSTVRLDVSY -> D (in isoform 2).
FT FTId=VSP 002559.
FT VARSPLIC 416 499 GLTESKWKGNELKPPPPAVAPSSGEGELHLYATLSFHKVK
FT PQPQCEADSEYSEIKHKHRETAQCLRNHPSPKEV
FT RG -> VSDVGFSTSIQPHL (in isoform 3).
FT FTId=VSP 002560.
SQ SEQUENCE 499 AA; 54042 MW; 086EFF989B74123C CRC64;

Query Match 35.0%; Score 947; DB 1; Length 499;
Best Local Similarity 42.1%; Pred. No. 2.9e-56;
Matches 223; Conservative 70; Mismatches 161; Indels 76; Gaps 13;

QY 1 MLPLLLSLGGSQAMDG-----RFWIRVQESVMVPEGLCISVPCSFSPRODWTGST 54
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MLLLLLLLPMLWTKMGEGDQVGYGLQVQLVQVGLCVHVPSCSFYQDQWTDSD 60
|||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 55 PAYGVYKAVETTKAPVATNQHSEVEMSTRGRFQLTGDPKAGNCSLVIRDAQWQDES 114
|||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 PVHGYWFRAGDRPYQAPVATNPDREVAQETQGRFQLLGDWNSDCSLSDARKDRKG 120
|||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 115 QVFFRVERGSY-----VRYNFMMDGFFLKVLTALQKPDVYIETLEPGQPVTVICVFNWA 169
|||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 121 SYFFRLERGMKWSYKSLNYKTQLSVFVTALTHTPEPDLILGLTLESHSRNLTCSPWA 180
|||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 170 FEECPSPSTWGAALSSOGTKPTTSHFVLSEFTTPAPQDHTDLTCHVDFFSRKGVSAQRT 229
|||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 181 CKQGTPTMISWIGASVSGF--PTTARSSVLTLTPKPDQGTSLTCQVTLPGTVTTST 238
|||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 230 VRLRVAYAPRDLVISRDNDPDPENLRVMVVSQANRTVLENLGNTSLPVLEGOSLCIV 289
|||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 239 VRLDVSY-----PPNLTWTVFQGDATASTALNGSSLSVLEGOSLRV 282
|||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 290 CVHTHSPPARLWQRTQGVLSQSPSDPGVLELPVQVHEGEFTCHARHPLGSHVLSL 349
|||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 283 CAVNSNPRLWTRGSLTLCFSRSSNPGLLEPRVHVHVEDEGFTCRAGNAQGSQHISLS 342
|||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 350 LSHYKKGILSTAFSN---GAPLIGITALLFL--CLALIMKILPKRTQTOTETPRPFS 404
|||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 343 LSLQNEGTGTSRPVSQVTLAAVGGAGATALLAFSLFCIIIV-----RSCRKKSARPAAG 397
|||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 405 RHSTILDYINVV---PTAGPLAQKRNQKATPSPRTPLPPGAPSPESKKNQKQKQLPSF 461
|||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 398 VGDGTGMDAKAIRGSASQGLTESKMD---GNPLKKPPAV-----435
|||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 462 PEKPSQTAPESQESGELHYATNLNPPGVPR-PEARMPKGTQADYAEVK 510
|||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 436 -----APSSGE-EGELHYATLSFHKVKPDQPGQ--EATDSEYSEIK 474
|||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 10
SILL_HUMAN
ID SILL_HUMAN STANDARD; PRT; 595 AA.
AC Q96PQ1; Q81YH7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Sialic acid binding Ig-like lectin-like 1 precursor (Siglec-like
molecule 1) (Siglec-L1) (UNQ9215/PRO34042).
GN Name=SIGLECU1; Synonyms=SLG;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC TISSUE=Bone marrow;
RX MEDLINE=21303046; PubMed=11409877; DOI=10.1006/bbrc.2001.5052;
RA Fousias G., Taylor S.M., Yousef G.M., Tropak M.B., Ordon M.H.,
RA Diamandis E.P.;
```

```
RT "Cloning and molecular characterization of two splice variants of a
new putative member of the Siglec-3-like subgroup of Siglecs."
RL Biochem. Biophys. Res. Commun. 284:887-899(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RX MEDLINE=21523976; PubMed=11546777; DOI=10.1074/jbc.M105926200;
RA Angata T., Varki N.M., Varki A.;
RT "A second uniquely human mutation affecting sialic acid biology."
RL J. Biol. Chem. 276:40282-40287(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment."
RL Genome Res. 13:2265-2270(2003).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC TISSUE=Blood.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell I.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Putative adhesion molecule that mediates sialic-acid
dependent binding to cells. The sialic acid recognition site may
be masked by cis interactions with sialic acids on the same cell
surface.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long; Synonyms=SLG-L;
CC IsoId=Q96PQ1-1; Sequence=Displayed;
CC Name=Short; Synonyms=SLG-S;
CC IsoId=Q96PQ1-2; Sequence=VSP 002566;
CC -!- TISSUE SPECIFICITY: The short isoform is highly expressed in
spleen, small intestine and adrenal gland; it is lower expressed
in thymoid, placenta, brain, stomach, bone marrow, spinal chord and
beast. The long isoform is highly expressed in spleen, small
intestine and bone marrow; it is lower expressed in thymoid,
placenta, thymus, trachea, stomach, lung, adrenal gland, fetal
brain and testis.
CC -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to
as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This
motif is involved in modulation of cellular responses. The
phosphorylated ITIM motif can bind the SH2 domain of several SH2-
containing phosphatases.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
```

(sialic acid binding Ig-like lectin) family.

-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

-!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.

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EMBL; AF277806; AAK51233.1; -
EMBL; AF277806; AAK51234.1; -
EMBL; AF282256; AAK71521.1; -
EMBL; AY358140; AAK88507.1; -
EMBL; BC035809; AAK35809.2; -
HSP; Q9Y286; 107S.
Genew; HGNC:15482; SIGLECL1.
MIM: 606094; -
InterPro: IPR007110; Ig-like.
Pfam: PF00047; ig; 4.
PROSITE; PSS0835; IG_LIKE; 3.
Alternative splicing; Cell adhesion; Glycoprotein;
Immunoglobulin domain; Lectin; Polymorphism; Repeat; Signal;
Transmembrane.
SIGNAL 1 18 Potential.
CHAIN 19 595 Sialic acid binding Ig-like lectin-like
DOMAIN 19 481 Extracellular (Potential).
TRANSMEM 482 502 Potential.
DOMAIN 503 595 Cytoplasmic (Potential).
DOMAIN 19 142 Ig-like V-type 1.
DOMAIN 143 269 Ig-like V-type 2.
DOMAIN 275 358 Ig-like C2-type 1.
DOMAIN 365 462 Ig-like C2-type 2.
DOMAIN 563 568 ITIM motif.
SITE 586 591 SLAM-LIKE MOTIF.
DISULFID 44 104 By similarity.
DISULFID 166 299 By similarity.
DISULFID 171 231 By similarity.
DISULFID 293 342 By similarity.
DISULFID 401 446 By similarity.
CARBOHYD 140 140 N-linked (GlcNAc...) (Potential).
CARBOHYD 179 179 N-linked (GlcNAc...) (Potential).
CARBOHYD 230 230 N-linked (GlcNAc...) (Potential).
CARBOHYD 290 290 N-linked (GlcNAc...) (Potential).
CARBOHYD 360 360 N-linked (GlcNAc...) (Potential).
CARBOHYD 367 367 N-linked (GlcNAc...) (Potential).
CARBOHYD 385 385 N-linked (GlcNAc...) (Potential).
VARSPIC 4 141
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NMKNVYDQLSVNV -> PLLWANEEDSGGWADPRFS
(in isoform Short).
/FTID=VSP_002566.
P -> T (in dBSNP:2034891).
/FTID=VAR_014259.
R -> W (in Ref. 3).
VARIANT 81 81
CONFLICT 528 528
SEQUENCE 595 AA; 64984 MW; D05662176274C5C3 CRC64;
Query Match 33.6%; Score 909; DB 1; Length 595;
Best Local Similarity 43.1%; Pred. No. 1.4e-53;
Matches 211; Conservative 65; Mismatches 174; Indels 40; Gaps 10;
7 LSSLGGSQAMGRFWIRVQSVNVPGLCISVPCFSFVPRQDWTGSTPAYWYFKAUTE 66
137 LSNVTASQDLLGRYLRLEVPSTVQGLCVSPVLYPHVNTWASSPVYGSWFKEGAD 196
67 TTKGAPVATNHQREVMSTFRGFQLTGDPKAGKNCSLVIRDAQMDESQYFFRVERGSV 126
197 IPWDIPVATNTPSGKQVQETHGFLFLGDDQTNWCSLSIRDAKSGDKYQVGRGSR- 255

QY 127 RYNEWMDGFFRLKVTALTQKPDVWIPETLEPGOPVTVICVENWAFEECPFPFSFWTGAALS 186
DB 256 KWNVIYDKLSVHVVALTHMTFTSIPGLESGHENLTCSVPWACEQGTPTITIMMGASVS 315
QY 187 SQGKPTTSHFSVLSTFTFPQDHDITDCHVDFSRKGVSAQRTVRLRVAYAPDLVISIS 246
DB 316 S--LDPTITRSSMLSLIPQPDHGTSLTQVTLPGAGVTMTAVRLNISV----- 363
QY 247 RNTFPDPENLRVMSQANRTVLENLNGTSLPVLGQSLCLVGVTHSSPPARLSWTORG 306
DB 364 -----PQNUTMTVFOGDGTASTTLRNGSALSVLGQSLHLVCAVDNSNPAPRLSWTWS 417
QY 307 QVLSFQSPDGVLEPRVQVEHEGFTCHARHPLGSHQVSLSLSVHYK---KGLISTAF 363
DB 418 LTLSPSQSSNLGVLEPRVHVWVDEGFTCAQNLPLGSHQVSLSLQNEVTKMRPISGV 477
QY 364 SNGAFLGIGITALLFLCLALIIIMKILPKRTQTETPPRPSRHSHTILDYINVV---PTAG 420
DB 478 TLGAFGGAGATALLVFLVFCIFVWV---RSCRKKSARPAVGVGTGMDANAVGASQSG 534
QY 421 PLACKRNOKATPNSPRTPLEP--CAPSPESKKNQKQVQLPSPFPPEPKSSTQAPESQESQE 478
DB 535 PLI-----ESPADDSPPHAPALATPSPE-----EGRIQVASLSFHKARPCYPOQEA-I 584
QY 479 ELHYATLNFP 488
DB 585 GYEYSEINIP 594
RESULT 11
SILL_PANTR
ID SILL_PANTR STANDARD; PRT; 597 AA.
AC Q95LH0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Sialic acid binding Ig-like lectin-like 1 precursor (Siglec-like molecule 1) (Siglec-L1).
GN Name=SIGLECL1;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_taxid=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21523976; PubMed=11546777; DOI=10.1074/jbc.M105926200;
RA Angata T., Varki N.M., Varki A.;
RT "A second uniquely human mutation affecting sialic acid biology.";
RL J. Biol. Chem. 276:40282-40287(2001).
CC -!- FUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. The sialic acid recognition site may be masked by cis interactions with sialic acids on the same cell surface.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in modulation of cellular responses. The phosphorylated ITIM motif can bind the SH2 domain of several SH2-containing phosphatases.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC (sialic acid binding Ig-like lectin) family.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
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